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=> s (integrating plasmid)

L1272 (INTEGRATING PLASMID)

=> s candida utilis

5634 CANDIDA UTILIS

=> s 12 and (biotin synthase)

11 L2 AND (BIOTIN SYNTHASE)

=> d 13 ti abs ibib tot

ANSWER 1 OF 11 USPATFULL on STN L3

TIMethods for monitoring multiple gene expression

The present invention relates to methods for monitoring differential AB expression of a plurality of genes in a first filamentous fungal cell relative to expression of the same genes in one or more second filamentous fungal cells using microarrays containing filamentous fungal expressed sequenced tags. The present invention also relates to filamentous fungal expressed sequenced tags and to computer readable media and substrates containing such expressed sequenced tags for monitoring expression of a plurality of genes in filamentous fungal cells.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

ACCESSION NUMBER: 2005:140340 USPATFULL

Methods for monitoring multiple gene expression TITLE: INVENTOR(S): Berka, Randy M., Davis, CA, UNITED STATES

Rey, Michael W., Davis, CA, UNITED STATES Shuster, Jeffrey R., Davis, CA, UNITED STATES

Kauppinen, Sakari, Smoerum, DENMARK Clausen, Ib Groth, Hillerod, DENMARK

Olsen, Peter Bjarke, Copenhagen, DENMARK

PATENT ASSIGNEE(S): Novozymes Biotech, Inc., Davis, CA, UNITED STATES (U.S.

corporation)

Novozymes A/S, Bagsvaerd, DENMARK (non-U.S.

corporation)

NUMBER KIND DATE -----US 6902887 B1 20050607 PATENT INFORMATION: APPLICATION INFO.: US 2000-533559 20000322 (9)

RELATED APPLN. INFO.: Continuation-in-part of Ser. No. US 1999-273623, filed

on 22 Mar 1999, ABANDONED

DOCUMENT TYPE: Utility GRANTED FILE SEGMENT:

PRIMARY EXAMINER: Brusca, John S. LEGAL REPRESENTATIVE: Stames, Robert L.

NUMBER OF CLAIMS: 8 EXEMPLARY CLAIM:

NUMBER OF DRAWINGS: 0 Drawing Figure(s); 0 Drawing Page(s)

LINE COUNT: 18386

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

ANSWER 2 OF 11 USPATFULL on STN L3

ΤI Methods for monitoring multiple gene expression

The present invention relates to methods for monitoring differential AB expression of a plurality of genes in a first filamentous fungal cell relative to expression of the same genes in one or more second filamentous fungal cells using microarrays containing filamentous fungal expressed sequenced tags. The present invention also relates to filamentous fungal expressed sequenced tags and to computer readable media and substrates containing such expressed sequenced tags for monitoring expression of a plurality of genes in filamentous fungal cells.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

ACCESSION NUMBER:

2004:292283 USPATFULL

TITLE:

Methods for monitoring multiple gene expression

INVENTOR(S):

Berka, Randy M., Davis, CA, UNITED STATES Rey, Michael W., Davis, CA, UNITED STATES Shuster, Jeffrey R., Davis, CA, UNITED STATES

Kauppinen, Sakari, Smoerum, DENMARK Clausen, Ib Groth, Hillerod, DENMARK Olsen, Peter Bjarke, Copenhagen, DENMARK

PATENT ASSIGNEE(S):

Novozymes Biotech, Inc., Davis, CA (U.S. corporation) Novozymes A/S, Inc., Bagsvaerd, DENMARK (U.S.

corporation)

NUMBER KIND DATE ______ US 2004229367 A1 20041118 US 2003-653047 A1 20030829 (10)

PATENT INFORMATION: APPLICATION INFO.:

RELATED APPLN. INFO.:

Division of Ser. No. US 2000-533559, filed on 22 Mar

2000, PENDING Continuation-in-part of Ser. No. US

1999-273623, filed on 22 Mar 1999, ABANDONED

DOCUMENT TYPE:

Utility

FILE SEGMENT:

APPLICATION

LEGAL REPRESENTATIVE:

NOVOZYMES BIOTECH, INC., 1445 DREW AVE, DAVIS, CA,

95616

NUMBER OF CLAIMS:

EXEMPLARY CLAIM:

8 1

LINE COUNT:

19697

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

ANSWER 3 OF 11 USPATFULL on STN L3

ΤI Yeast with high biotin-productivity and the preparation method thereof The invention discloses a yeast with high biotin-productivity and the AB preparation method thereof. The yeast is transformed by an integrated plasmid, which includes a biotin synthase gene, an assistant DNA sequence for the integration of the plasmid into a host

genome, a promoter sequence, and a selection marker.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

ACCESSION NUMBER:

2003:152918 USPATFULL

TITLE:

Yeast with high biotin-productivity and the preparation

method thereof

INVENTOR(S):

Shiuan, David, Kaohsiung, TAIWAN, PROVINCE OF CHINA

KIND NUMBER DATE US 2003104584 A1 20030605 US 2001-752957 A1 20010102 (9) PATENT INFORMATION: APPLICATION INFO.:

NUMBER DATE

PRIORITY INFORMATION: TW 2000-89120972 20001007

DOCUMENT TYPE: Utility FILE SEGMENT: APPLICATION

LEGAL REPRESENTATIVE: BRUCE LONDA, NORRIS, MCLAUGHLIN & MARCUS, P.A., 220

EAST 42ND STREET, 30TH FLOOR, NEW YORK, NY, 10017

NUMBER OF CLAIMS: 16 EXEMPLARY CLAIM: 1

NUMBER OF DRAWINGS: 13 Drawing Page(s)

LINE COUNT: 486

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L3 ANSWER 4 OF 11 USPATFULL on STN

TI Novel Polynucleotides

AB Novel polynucleotides derived from microorganisms belonging to coryneform bacteria and fragments thereof, polypeptides encoded by the polynucleotides and fragments thereof, polynucleotide arrays comprising the polynucleotides and fragments thereof, recording media in which the nucleotide sequences of the polynucleotide and fragments thereof have been recorded which are readable in a computer, and use of them.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

ACCESSION NUMBER: 2002:343879 USPATFULL TITLE: Novel Polynucleotides

INVENTOR(S): Nakagawa, Satoshi, Tokyo, JAPAN Mizoguchi, Hiroshi, Tokyo, JAPAN

Ando, Seiko, Tokyo, JAPAN
Hayashi, Mikiro, Tokyo, JAPAN
Ochiai, Keiko, Tokyo, JAPAN
Yokoi, Haruhiko, Tokyo, JAPAN
Tateishi, Naoko, Tokyo, JAPAN
Senoh, Akihiro, Tokyo, JAPAN

Ikeda, Masato, Tokyo, JAPAN Ozaki, Akio, Hofu-shi, JAPAN

KENID

	NUMBER		DAIE	
		-		
PATENT INFORMATION:	US 2002197605	A1	20021226	
APPLICATION INFO.:	US 2000-738626	A1	20001218	(9)

MI IMPER

		NUMBER	DATE
PRIORITY	INFORMATION:	JP 1999-377484	19991216
		JP 2000-159162 JP 2000-280988	20000407 20000803

DOCUMENT TYPE: Utility
FILE SEGMENT: APPLICATION

LEGAL REPRESENTATIVE: NIXON & VANDERHYE P.C., 8th Floor, 1100 North Glebe

Road, Arlington, VA, 22201

NUMBER OF CLAIMS: 68 EXEMPLARY CLAIM: 1

NUMBER OF DRAWINGS: 4 Drawing Page(s)

LINE COUNT: 13673

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L3 ANSWER 5 OF 11 DGENE COPYRIGHT 2005 The Thomson Corp on STN

TI New integrated plasmid, useful for preparing yeast with high biotinproductivity used as feed additives, food additives or cosmetics.

AN ADA09589 DNA DGENE

AB The present invention relates to a yeast with high biotin-productivity and a method for its preparation. The yeast is transformed by an integrated plasmid, which includes the edible yeast (Candida utilis) biotin synthase gene, an assistant

DNA sequence for the integration of the plasmid into a host genome, a promoter sequence, and a selection marker. The prepared yeast with high biotin-productivity or recovered biotin is useful as feed additives, food additives or cosmetics. The present sequence represents a PCR primer used in the examples of the present invention.

ACCESSION NUMBER: ADA09589 DNA DGENE

TITLE: New integrated plasmid, useful for preparing yeast with high

biotin- productivity used as feed additives, food additives

or cosmetics.

INVENTOR: Shiuan D

PATENT ASSIGNEE: (SHIU-I) SHIUAN D.

PATENT INFO: US 2003104584 A1 20030605 20

APPLICATION INFO: US 2001-752957 20010102 PRIORITY INFO: TW 2000-120972 20001007

DOCUMENT TYPE: Patent LANGUAGE: English

OTHER SOURCE: 2003-567956 [53]

DESCRIPTION: PCR primer #1 for S. cerevisiae BIO2 gene.

L3 ANSWER 6 OF 11 DGENE COPYRIGHT 2005 The Thomson Corp on STN

TI New integrated plasmid, useful for preparing yeast with high biotinproductivity used as feed additives, food additives or cosmetics.

AN ADA09591 DNA DGENE

AB The present invention relates to a yeast with high biotin-productivity and a method for its preparation. The yeast is transformed by an integrated plasmid, which includes the edible yeast (Candida utilis) biotin synthase gene, an assistant

DNA sequence for the integration of the plasmid into a host genome, a promoter sequence, and a selection marker. The prepared yeast with high biotin-productivity or recovered biotin is useful as feed additives, food additives or cosmetics. The present sequence represents a degenerate PCR primer used in the examples of the present invention.

ACCESSION NUMBER: ADA09591 DNA DGENE

TITLE: New integrated plasmid, useful for preparing yeast with high

biotin- productivity used as feed additives, food additives

or cosmetics.

INVENTOR: Shiuan D

PATENT ASSIGNEE: (SHIU-I)SHIUAN D.

PATENT INFO: US 2003104584 A1 20030605 20

APPLICATION INFO: US 2001-752957 20010102 PRIORITY INFO: TW 2000-120972 20001007

DOCUMENT TYPE: Patent LANGUAGE: English

OTHER SOURCE: 2003-567956 [53]

DESCRIPTION: Degenerate PCR primer #1 for C. utilis BIO2 gene.

L3 ANSWER 7 OF 11 DGENE COPYRIGHT 2005 The Thomson Corp on STN

TI New integrated plasmid, useful for preparing yeast with high biotinproductivity used as feed additives, food additives or cosmetics.

AN ADA09590 DNA DGENE

AB The present invention relates to a yeast with high biotin-productivity and a method for its preparation. The yeast is transformed by an integrated plasmid, which includes the edible yeast (Candida utilis) biotin synthase gene, an assistant

DNA sequence for the integration of the plasmid into a host genome, a promoter sequence, and a selection marker. The prepared yeast with high biotin-productivity or recovered biotin is useful as feed additives, food additives or cosmetics. The present sequence represents a PCR primer used in the examples of the present invention.

ACCESSION NUMBER: ADA09590 DNA DGENE

TITLE: New integrated plasmid, useful for preparing yeast with high biotin- productivity used as feed additives, food additives

or cosmetics.

INVENTOR: Shiuan D

PATENT ASSIGNEE: (SHIU-I) SHIUAN D.

PATENT INFO: US 2003104584 A1 20030605 20

APPLICATION INFO: US 2001-752957 20010102 PRIORITY INFO: TW 2000-120972 20001007

DOCUMENT TYPE: Patent LANGUAGE: English

OTHER SOURCE: 2003-567956 [53]

DESCRIPTION: PCR primer #2 for S. cerevisiae BIO2 gene.

.L3 ANSWER 8 OF 11 DGENE COPYRIGHT 2005 The Thomson Corp on STN

TI New integrated plasmid, useful for preparing yeast with high biotinproductivity used as feed additives, food additives or cosmetics.

AN ADA09592 DNA DGENE

AB The present invention relates to a yeast with high biotin-productivity and a method for its preparation. The yeast is transformed by an integrated plasmid, which includes the edible yeast (Candida utilis) biotin synthase gene, an assistant

DNA sequence for the integration of the plasmid into a host genome, a promoter sequence, and a selection marker. The prepared yeast with high biotin-productivity or recovered biotin is useful as feed additives, food additives or cosmetics. The present sequence represents a

degenerate PCR primer used in the examples of the present invention.

ACCESSION NUMBER: ADA09592 DNA DGENE

TITLE: New integrated plasmid, useful for preparing yeast with high

biotin- productivity used as feed additives, food additives

or cosmetics.

INVENTOR: Shiuan D

PATENT ASSIGNEE: (SHIU-I) SHIUAN D.

PATENT INFO: US 2003104584 A1 20030605 20

APPLICATION INFO: US 2001-752957 20010102 PRIORITY INFO: TW 2000-120972 20001007

DOCUMENT TYPE: Patent LANGUAGE: English

OTHER SOURCE: 2003-567956 [53]

DESCRIPTION: Degenerate PCR primer #2 for C. utilis BIO2 gene.

L3 ANSWER 9 OF 11 DGENE COPYRIGHT 2005 The Thomson Corp on STN

TI New integrated plasmid, useful for preparing yeast with high biotinproductivity used as feed additives, food additives or cosmetics.

AN ADA09588 DNA DGENE

The present invention relates to a yeast with high biotin-productivity and a method for its preparation. The yeast is transformed by an integrated plasmid, which includes the edible yeast (Candida utilis) biotin synthase gene, an assistant

DNA sequence for the integration of the plasmid into a host genome, a promoter sequence, and a selection marker. The prepared yeast with high biotin-productivity or recovered biotin is useful as feed additives, food additives or cosmetics. The present sequence represents C. utilis

biotin synthase gene.

ACCESSION NUMBER: ADA09588 DNA DGENE

TITLE: New integrated plasmid, useful for preparing yeast with high

biotin- productivity used as feed additives, food additives

or cosmetics.

INVENTOR: Shiuan D

PATENT ASSIGNEE: (SHIU-I) SHIUAN D.

PATENT INFO: US 2003104584 A1 20030605 20

APPLICATION INFO: US 2001-752957 20010102 PRIORITY INFO: TW 2000-120972 20001007

DOCUMENT TYPE: Patent LANGUAGE: English

OTHER SOURCE: 2003-567956 [53]
DESCRIPTION: Candida utilis biotin

synthase gene.

L3 ANSWER 10 OF 11 WPIDS COPYRIGHT 2005 THE THOMSON CORP on STN

TI New integrated plasmid, useful for preparing yeast with high

biotin-productivity used as feed additives, food additives or cosmetics.

AN 2003-567956 [53] WPIDS

AB US2003104584 A UPAB: 20030820

NOVELTY - An integrated plasmid comprising a **biotin synthase** gene, an assistant DNA sequence for the integration of the plasmid into a host genome, a promoter sequence, and a selection marker, is new.

 ${\tt DETAILED}$ <code>DESCRIPTION</code> - <code>INDEPENDENT</code> <code>CLAIMS</code> are included for the following:

- (1) a method for preparing a yeast with high biotin-productivity comprising constructing the integrated plasmid cited above, linearizing the integrated plasmid, transforming the linearized integrated plasmid into a yeast, and recombining the **biotin synthase** gene with the yeast genome; and
- (2) a method for producing biotin comprising providing the yeast with high biotin-productivity, culturing the yeast in a nutrient medium, and recovering biotin from the culture broth.

USE - The integrated plasmid is useful for preparing yeast with high biotin-productivity. The prepared yeast with high biotin-productivity or recovered biotin is useful as feed additives, food additives or cosmetics (all claimed).

Dwg.0/13

ACCESSION NUMBER:

2003-567956 [53] WPIDS

DOC. NO. CPI:

C2003-153236

TITLE:

New integrated plasmid, useful for preparing yeast with

high biotin-productivity used as feed additives, food

additives or cosmetics.

DERWENT CLASS:

C06 D13 D16 D21

INVENTOR(S):

SHIUAN, D

PATENT ASSIGNEE(S):

(NASC-N) NAT SCI COUNCIL: (SHIU-I) SHIUAN D

COUNTRY COUNT:

PATENT INFORMATION:

PATENT NO	KIND DATE	WEEK	LA PG
US 2003104584 TW 220675	A1 20030605 B1 20040901		20

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
US 2003104584	A1	US 2001-752957	20010102
TW 220675	B1	TW 2000-120972	

PRIORITY APPLN. INFO: TW 2000-120972 20001007

ANSWER 11 OF 11 BIOTECHDS COPYRIGHT 2005 THE THOMSON CORP. on STN New integrated plasmid, useful for preparing yeast with high

New integrated plasmid, useful for preparing yeast with high biotin-productivity used as feed additives, food additives or cosmetics:

vector-mediated gene transfer and expression in host cell for strain improvement and feed additive, food additive or cosmetic manufacture

AN 2003-20688 BIOTECHDS

AB DERWENT ABSTRACT:

NOVELTY - An integrated plasmid comprising a **biotin synthase** gene, an assistant DNA sequence for the integration of the plasmid into a host genome, a promoter sequence, and a selection marker, is new.

DETAILED DESCRIPTION - INDEPENDENT CLAIMS are included for the following: (1) a method for preparing a yeast with high biotin-productivity comprising constructing the integrated plasmid cited above, linearizing the integrated plasmid, transforming the linearized integrated plasmid into a yeast, and recombining the biotin synthase gene with the yeast genome; and (2) a method for producing biotin comprising providing the yeast with high biotin-productivity, culturing the yeast in a nutrient medium, and recovering biotin from the culture broth.

BIOTECHNOLOGY - Preferred Plasmid: The biotin synthase gene of the integrated plasmid is derived from Saccharomyces cerevisiae or Candida utilis. The biotin synthase gene of C. utilis comprises a fully defined sequence of 1188 base pairs (bp) given in the specification. The assistant DNA sequence is a C. utilis fragment consisting of NsiI-BamHI 18s rDNA, URA3 DNA, or HIS3 DNA. The selection marker is preferably a cycloheximide-resistant gene. The promoter sequence is pL41 promoter of C. utilis or pADH1 promoter of S. cerevisiae. The integrated plasmid is: (A) pMCC21 comprising pL41 for the expression of C. utilis BIO2 gene encoding for 204 amino acids, mutated L41 gene used as cycloheximide-resistant marker, and C. utilis 18S rDNA; (B) pMCC31S or pMCC38S comprising pL41 for the expression of C. utilis BIO2 gene encoding for 233 amino acids, mutated L41 gene used as cycloheximide-resistant marker, and C. utilis 18S rDNA; (C) pMCC32H or pMCC36H comprising C. utilis pL41, C. utilis BIO2 gene, mutated L41 gene used as cycloheximide-resistant marker, and C. utilis HIS3 gene fragment; or (D) pMCC33U or pMCC35U comprising C. utilis pL41, C. utilis BIO2 gene, mutated L41 gene used as cycloheximide-resistant marker, and C. utilis URA3 gene fragment.

USE - The integrated plasmid is useful for preparing yeast with high biotin-productivity. The prepared yeast with high biotin-productivity or recovered biotin is useful as feed additives, food additives or cosmetics (all claimed).

EXAMPLE - Polymerase chain reaction (PCR) was carried out using the Candida utilis BIO2 gene as a template. The product was digested with NdeI and SalI, and ligated into pMC5 to obtain pMCC11. The NdeI-SalI fragment of pMCC11 in which the NdeI nickel was end-repaired into a blunt end by Klenow DNA polymerase (i.e. pL41-BIO2 fragment) was ligated into pMC9 to obtain pMCC15. To fill the lost L41 fragment, the BamHI-EcoRI fragment of pMC9 (i.e. L41 gene fragment) was end-repaired into a blunt end by Klenow DNA polymerase and then integrated into the SalI site in pMCC15 to obtain pMCC21. The plasmid pMCC21 comprises C. utilis pL41 for the expression of the C. utilis BIO2 gene, mutated L41 gene used as cycloheximide-resistant marker, and C. utilis 18S rDNA. (20 pages)

ACCESSION NUMBER: 2003-20688 BIOTECHDS

TITLE: New integrated plasmid, useful for preparing yeast with high

biotin-productivity used as feed additives, food additives or.

cosmetics;

vector-mediated gene transfer and expression in host cell for strain improvement and feed additive, food additive or

cosmetic manufacture

AUTHOR: SHIUAN D PATENT ASSIGNEE: SHIUAN D

PATENT INFO: US 2003104584 5 Jun 2003 APPLICATION INFO: US 2001-752957 2 Jan 2001

PRIORITY INFO: TW 2000-120972 7 Oct 2000; TW 2000-120972 7 Oct 2000

DOCUMENT TYPE: Patent LANGUAGE: English

OTHER SOURCE: WPI: 2003-567956 [53]

ΤI

AB

=> s 14 and (biotin production)

L5 0 L4 AND (BIOTIN PRODUCTION)

=> s 14 and (biotin)

L6 8 L4 AND (BIOTIN)

=> d 16 ti abs ibib tot

L6 ANSWER 1 OF 8 USPATFULL on STN

Whole cell engineering using real-time metabolic flux analysis
The invention provides methods for whole cell engineering of new and
modified phenotypes by using "on-line" or "real-time" metabolic flux
analysis. The invention provides a method for whole cell engineering of
new or modified phenotypes by using real-time metabolic flux analysis by
making a modified cell by modifying the genetic composition of a cell
and culturing the modified cell to generate a plurality of modified
cells and measuring at least one metabolic parameter of the cell by
monitoring the cell culture of in real time. The invention also provides
articles comprising machine-readable medium including machine-executable
instructions and systems, e.g., computer systems, to practice the

ACCESSION NUMBER: 2005:233489 USPATFULL

methods of the invention.

TITLE: Whole cell engineering using real-time metabolic flux

analysis

INVENTOR(S): Short, Jay M., Rancho Sante Fe, CA, UNITED STATES

Latterich, Martin, Montreal, CANADA

Levin, Michael, San Diego, CA, UNITED STATES Wei, Jing, San Diego, CA, UNITED STATES Fu, Pengcheng, Honolulu, HI, UNITED STATES

20050223 PCT 371 date

US 2003-326654P 20011001 (60) US 2003-326655P 20011001 (60) US 2003-337526P 20011109 (60)

DOCUMENT TYPE: Utility FILE SEGMENT: APPLICATION

LEGAL REPRESENTATIVE: DIVERSA C/O MOFO S.D., 3811 VALLEY CENTER DRIVE, SUITE

500, SAN DIEGO, CA, 92130, US

NUMBER OF CLAIMS: 80

EXEMPLARY CLAIM: 1

NUMBER OF DRAWINGS: 40 Drawing Page(s)

LINE COUNT: 4859

L6 ANSWER 2 OF 8 USPATFULL on STN

TI Screening method for genes of brewing yeast

AB The present invention provides (A) a method for the selection of genes participating in the desired brewing character, which comprises preparing a database compiling the data of the whole genome sequence of industrial yeast, particularly a brewing yeast used for alcoholic beverages; selecting gene participating in a desired brewing character that the brewing yeast specifically possesses; and carrying out

functional analysis of the gene by disruption or overexpression; (B) a DNA array in which oligonucleotide(s) selected based on the data base compiling the data of the whole genome sequences of an industrial yeast, (C) a breeding method for constructing improved cultures achieving the desired brewing character, (D) a method for producing an alcohol or an alcoholic beverage in which productivity and quality are improved using the yeast, (E) a gene which is specific to the improved brewing yeast, and (F) a peptide encoded by the gene.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

ACCESSION NUMBER: 2004:334780 USPATFULL

TITLE:

Screening method for genes of brewing yeast

INVENTOR(S):

Nakao, Yoshihiro, Kyoto-shi, JAPAN Nakamura, Norihisa, Kyoto-shi, JAPAN

Kodama, Yukiko, Osaka, JAPAN Fujimura, Tomoko, Osaka, JAPAN Ashikari, Toshihiko, Osaka, JAPAN

PATENT ASSIGNEE(S):

SUNTORY LIMITED, OSAKA, JAPAN (non-U.S. corporation)

KIND DATE NUMBER -----

PATENT INFORMATION: US 2004265862 A1 20041230 APPLICATION INFO.: US 2004-791791 A1 20040304 (10)

NUMBER DATE ------

PRIORITY INFORMATION:

Utility

JP 2003-57677 20030304

DOCUMENT TYPE:

FILE SEGMENT:

APPLICATION

LEGAL REPRESENTATIVE: BURNS DOANE SWECKER & MATHIS L L P, POST OFFICE BOX

1404, ALEXANDRIA, VA, 22313-1404 .

NUMBER OF CLAIMS:

1

EXEMPLARY CLAIM:

12 Drawing Page(s)

NUMBER OF DRAWINGS: LINE COUNT:

3038

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L6 ANSWER 3 OF 8 USPATFULL on STN

ΤI Whole cell engineering using real-time metabolic flux analysis

AB The invention provides methods for whole cell engineering of new and modified phenotypes by using "on-line" or "real-time" metabolic flux analysis. The invention provides a method for whole cell engineering of new or modified phenotypes by using real-time metabolic flux analysis by making a modified cell by modifying the genetic composition of a cell and culturing the modified cell to generate a plurality of modified cells and measuring at least one metabolic parameter of the cell by monitoring the cell culture of in real time. The invention also provides articles comprising machine-readable medium including machine-executable instructions and systems, e.g., computer systems, to practice the methods of the invention.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

ACCESSION NUMBER:

PATENT ASSIGNEE(S):

2004:44982 USPATFULL

TITLE:

Whole cell engineering using real-time metabolic flux

analysis

INVENTOR(S):

Fu, Pengcheng, Honolulu, HI, UNITED STATES

Latterich, Martin, San Diego, CA, UNITED STATES Levin, Michael, San Diego, CA, UNITED STATES

Wei, Jing, San Diego, CA, UNITED STATES

Short, Jay M., Rancho Santa Fe, CA, UNITED STATES Diversa Corporation, San Diego, CA (U.S. corporation)

NUMBER KIND DATE PATENT INFORMATION:

US 2004033975 A1 20040219 US 2002-264989 A1 20021001 (10) APPLICATION INFO.:

DATE NUMBER

PRIORITY INFORMATION:

US 2001-326655P 20011001 (60) US 2001-326654P 20011001 (60) US 2001-326653P 20011001 (60) US 2001-337526P 20011109 (60)

DOCUMENT TYPE: Utility FILE SEGMENT: APPLICATION

LEGAL REPRESENTATIVE: GREGORY P. EINHORN, Fish & Richardson P.C., Suite 500,

4350 La Jolla Village Drive, San Diego, CA, 92122

NUMBER OF CLAIMS: EXEMPLARY CLAIM:

NUMBER OF DRAWINGS: 40 Drawing Page(s)

LINE COUNT: 5427

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

ANSWER 4 OF 8 USPATFULL on STN L6

TT Baker's yeast and a method producing it

A process is disclosed for the production of baker's yeast which AB comprises the fermentation of a baker's yeast strain using a non-molasses carbon source until a fermentation broth having at least 10%, preferably at least 13%, more preferably at least 16% of dry solids content is formed, which can be used directly as a cream yeast without concentration.

ACCESSION NUMBER: 1999:72304 USPATFULL

Baker's yeast and a method producing it TITLE:

Plomp, Pieter Jan Arnoldus Maria, Ex Delft, Netherlands INVENTOR(S):

PATENT ASSIGNEE(S): Gist-brocades, B.V., Netherlands (non-U.S. corporation)

> NUMBER KIND DATE -----

PATENT INFORMATION:

US 5916609 19990629 19970728 (8) US 1997-901312 APPLICATION INFO.:

NUMBER DATE -----EP 1996-202119 19960727

PRIORITY INFORMATION: DOCUMENT TYPE: Utility

FILE SEGMENT: Granted

Granteu Sayala, Chhaya D. PRIMARY EXAMINER:

LEGAL REPRESENTATIVE: Morrison & Foerster, LLP

NUMBER OF CLAIMS: 21 EXEMPLARY CLAIM: 1 LINE COUNT: 537

1.6 ANSWER 5 OF 8 USPATFULL on STN

ΤI Production of distillers yeast

AB Distillers yeast is produced by a process which results in more rapid yeast growth, higher cell concentrations and greatly extended yeast viability. The process involves propagating yeast on a culture medium of cooked cereal grain mash which has been subjected to enzymatic action of glucamylase obtained from fungi of the genus Aspergillus. After propagation, as a result of substantially longer viability, the yeast can be stored in the culture medium for up to 3 days or longer with portions being withdrawn from time to time for inoculating distillery grain mashes.

75:10033 USPATFULL ACCESSION NUMBER:

Production of distillers yeast TITLE:

Van Lanen, deceased, James M., late of Peoria, IL, INVENTOR (S):

United States

Smith, Merritt B., Peoria, IL, United States Maisch, Weldon F., Peoria, IL, United States

PATENT ASSIGNEE(S): Hiram Walker & Sons, Inc., Peoria, IL, United States

(U.S. corporation)

NUMBER KIND DATE

PATENT INFORMATION:

US 3868307 19750225 US 1973-388359 19730815

APPLICATION INFO.: RELATED APPLN. INFO.: Continuation-in-part of Ser. No. US 1971-189678, filed

on 15 Oct 1971, now abandoned

DOCUMENT TYPE:

FILE SEGMENT: Granted

PRIMARY EXAMINER: Naff, David M. LEGAL REPRESENTATIVE: Kirkland and Ellis

NUMBER OF CLAIMS: EXEMPLARY CLAIM: 1

2 Drawing Figure(s); 2 Drawing Page(s) NUMBER OF DRAWINGS:

LINE COUNT: 633

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

1.6 ANSWER 6 OF 8 WPIDS COPYRIGHT 2005 THE THOMSON CORP on STN

Bread-baking yeast preparation - involves adding aryl-thioacetic acid derivs. TIto des thio-biotin used in molasses-based nutrient medium for yeast cultivation.

1988-159690 [23] WPIDS AN

1350172 A UPAB: 19930923 AB

> The bread-baking yeasts are obtd. by multistage cultivation under aeration conditions on a nutrient medium containing molasses, mineral salts and desthiobiotin. During the stages of production of yeast inoculant and commercial yeasts, derivs. of arylthio (sulphonyl) acetic acid are added in amount (1-10000)x10 power minus 10% jointly with desthiobiotin.

The specified derivs. are 2-hydroxyalkyl-ammonium salts of formula (I), where (a) R=H, R2=4CH3, n=2 and X=N+H3CH(CH2OH)CH(OH)C6H4NO2-4; (b) R1=H, R2=4C1, n=0 and X=N+H(CH3)2CH2CH2OH; or (c) R1=H, R2=4C1, n=2, and X=N+H (CH2CH2OH) 3.

(I) contain metabolically active sulphur which can be incorporated into desthiobiotin and form biotin. (I) also act as antioxidants by lowering the intensity of peroxide oxidation of lipids of biological membranes.

USE/ADVANTAGE - In the microbiological industry. Increased biomass yield is obtd. Bul.41/7.11.87

0/0

ACCESSION NUMBER: 1988-159690 [23] WPIDS

DOC. NO. CPI: C1988-071563

TITLE: Bread-baking yeast preparation - involves adding

aryl-thioacetic acid derivs. to des thio-biotin used in molasses-based nutrient medium for yeast cultivation.

D11 D16 E19

DERWENT CLASS:

GUSEVA, S A; LEVKOVSKAY, G G; MIRSKOVA, A N INVENTOR(S):

(ASII) AS SIBE IRKUT ORG CHEM; (BREA) LENGD BREAD BAKING PATENT ASSIGNEE(S):

COUNTRY COUNT: 1

PATENT INFORMATION:

PATENT NO KIND DATE WEEK LA PG ______ SU 1350172 A 19871107 (198823)* 3

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE		
SU 1350172	A	SU 1985-3960649	19851005		

PRIORITY APPLN. INFO: SU 1985-3960649 19851005

L6 ANSWER 7 OF 8 WPIDS COPYRIGHT 2005 THE THOMSON CORP on STN

TI Yeast prepared by culturing Hansenula ofunaensis - in medium containing methanol, ethanol and/or glucose as carbon source.

AN 1978-02953A [02] WPIDS

AB JP 52139773 A UPAB: 19930901

The method is characterised by culturing a novel yeast stock Hansenula of unaensis (FERM-P 3494). The yeast stock Hansenula of unaensis can utilise methanol, ethanol and glucose, which are favourable as the starting material for preparing yeast for food use.

The culture is practiced aerobically at 10-41 pref. 30-39 degrees C in the medium containing methanol, ethanol and/or glucose as carbon source at pH 2-9 pref. 3-7 for up to 6 days. As the growth promoter vitamins such as thiamine, biotin, etc. and amino acid such as methionine, cysteine, etc. can be applied. After the culture yeast body is separated washed and dried.

ACCESSION NUMBER:

1978-02953A [02] WPIDS

TITLE:

Yeast prepared by culturing Hansenula ofunaensis - in

medium containing methanol, ethanol and/or glucose as carbon

source.

DERWENT CLASS:

C03 D13 D16

PATENT ASSIGNEE(S):

(MITK) MITSUI TOATSU CHEM INC

COUNTRY COUNT:

1

PATENT INFORMATION:

PA.	TENT NO	KII	ND DATE	WEEK	LA	PG
JP	52139773		19771121	(197802)*		
JΡ	56012109	В	19810318	(198115)		

PRIORITY APPLN. INFO: JP 1976-44940 19760422

L6 ANSWER 8 OF 8 WPIDS COPYRIGHT 2005 THE THOMSON CORP on STN

TI Yeast preparation using Torulopsis methanothermophilus - in culture medium containing methanol as carbon source and **biotin**.

AN 1977-19283Y [11] WPIDS

AB JP 52015882 A UPAB: 19930901

Method is effected by inoculating a stock belonging to Torulopsis methanothermophilus which can utilize methanol, into a culture medium containing methanol as carbon source and **biotin**, culturing it for multiplication and separating the yeast body.

The stock can multiply at high temperature and low pH and is considered a novel stock. The stock is trusted to Institute of Microbial Industry with the Trust Number 3158. As teh carbon source crude methanol which contains small amount of lower aldehydes, lower alcohols, etc. can be used. With methanol concentrate >4% the growth of the yest is inhibited, so methanol is added to the culture medium little by little.

ACCESSION NUMBER:

1977-19283Y [11] WPIDS

TITLE:

Yeast preparation using Torulopsis methanothermophilus - in

culture medium containing methanol as carbon source and

biotin.

DERWENT CLASS:

D16

PATENT ASSIGNEE(S): (MITP) MITSUBISHI PETROCHEMICAL CO LTD

COUNTRY COUNT:

PATENT INFORMATION:

PATENT NO KIND DATE WEEK LA PG ------JP 52015882 A 19770205 (197711)*

PRIORITY APPLN. INFO: JP 1975-91807 19750728

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(FILE 'HOME' ENTERED AT 13:07:27 ON 20 SEP 2005)

FILE 'MEDLINE, USPATFULL, DGENE, EMBASE, WPIDS, BIOSIS, BIOTECHDS'

ENTERED AT 13:08:15 ON 20 SEP 2005

L1272 S (INTEGRATING PLASMID)

5634 S CANDIDA UTILIS L2

L3 11 S L2 AND (BIOTIN SYNTHASE)

T.4 310 S YEAST PREPARATION

0 S L4 AND (BIOTIN PRODUCTION) L5

8 S L4 AND (BIOTIN) L6

=> s l1 and l3

0 L1 AND L3 Ļ7

=> s 12 and 11

L8 2 L2 AND L1

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ANSWER 1 OF 2 USPATFULL on STN 1.8

TI Production of farnesol and geranylgeraniol

AB The invention provides a biological method of producing farnesol or geranylgeraniol.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

ACCESSION NUMBER: 2004:144592 USPATFULL

TITLE: INVENTOR (S):

Production of farnesol and geranylgeraniol Millis, James R., Kohler, WI, UNITED STATES

Maurina-Brunker, Julie, Appleton, WI, UNITED STATES McMullin, Thomas W., Manitowoc, WI, UNITED STATES

PATENT ASSIGNEE(S):

Arkion Life Sciences LLC. (U.S. corporation)

NUMBER KIND DATE -----

PATENT INFORMATION: APPLICATION INFO.:

US 2004110257 A1 20040610 US 2003-719196 A1 20031120 (10)

RELATED APPLN. INFO.:

Continuation of Ser. No. US 2001-909558, filed on 20 Jul 2001, GRANTED, Pat. No. US 6689593 Continuation of Ser. No. US 1999-350275, filed on 6 Jul 1999, GRANTED,

Pat. No. US 6531303

DATE NUMBER

PRIORITY INFORMATION:

-----US 1998-91964P 19980706 (60)

DOCUMENT TYPE:

Utility

FILE SEGMENT:

APPLICATION

LEGAL REPRESENTATIVE: SHERIDAN ROSS PC, 1560 BROADWAY, SUITE 1200, DENVER,

CO, 80202

NUMBER OF CLAIMS: 17 EXEMPLARY CLAIM: 1

NUMBER OF DRAWINGS: 11 Drawing Page(s)

LINE COUNT: 3450

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L8 ANSWER 2 OF 2 USPATFULL on STN

TI Manufacture of five-carbon sugars and sugar alcohols

AB The invention relates to the methods of manufacturing five-carbon sugars

and sugar alcohols as well as other compounds derived from

pentose-phosphate pathway from readily available substrates such a

hexoses using metabolically engineered microbial hosts.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

ACCESSION NUMBER:

2003:99684 USPATFULL

TITLE:

Manufacture of five-carbon sugars and sugar alcohols

INVENTOR(S):

Miasnikov, Andrei, Kantvik, FINLAND Ojamo, Heikki, Kirkkonummi, FINLAND Povelainen, Mira, Espoo, FINLAND Gros, Hakan, Kantvik, FINLAND Toivari, Mervi, Espoo, FINLAND Richard, Peter, Helsinki, FINLAND Ruohonen, Laura, Helsinki, FINLAND Koivuranta, Kari, Helsinki, FINLAND

Londesborough, John, Helsinki, FINLAND Aristidou, Aristos, Espoo, FINLAND Penttila, Merja, Helsinki, FINLAND Plazanet-Menut, Claire, Paris, FRANCE

Deutscher, Josef, Fontenay Le Fleury, FRANCE

PATENT ASSIGNEE(S):

Xyrofin Oy (non-U.S. corporation)

NUMBER KIND DATE
US 2003068791 A1 20030410
US 2001-908744 A1 20010720

PATENT INFORMATION: APPLICATION INFO.:

APPLICATION INFO.: US 2001-908744 A1 20010720 (9)
RELATED APPLN. INFO.: Continuation-in-part of Ser. No. US 2000-488581, filed

on 21 Jan 2000, ABANDONED Continuation-in-part of Ser. No. US 1997-790585, filed on 29 Jan 1997, PENDING

Continuation of Ser. No. US 1995-368395, filed on 3 Jan 1995, GRANTED, Pat. No. US 5631150 Continuation of Ser. No. US 1993-110672, filed on 24 Aug 1993, ABANDONED Continuation-in-part of Ser. No. US 1992-973325, filed on 5 Nov 1992, ABANDONED Continuation-in-part of Ser.

No. WO 2001-FI51, filed on 22 Jan 2001, UNKNOWN

DOCUMENT TYPE: Utility
FILE SEGMENT: APPLICATION

LEGAL REPRESENTATIVE: STERNE, KESSLER, GOLDSTEIN & FOX PLLC, 1100 NEW YORK

AVENUE, N.W., SUITE 600, WASHINGTON, DC, 20005-3934

NUMBER OF CLAIMS: 166

EXEMPLARY CLAIM: 1

NUMBER OF DRAWINGS: 25 Drawing Page(s)

LINE COUNT: 5422

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

=> file scisearch, biosis, medline, uspatful, wpids, biotechds, embase, dgene

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FULL ESTIMATED COST 86.18 86.39

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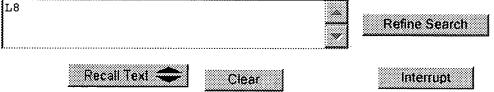
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US OCR Full-Text Database
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IBM Technical Disclosure Bulletins

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Database:



Search History

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<u>L5</u>	L4 and (yeast preparation)	76057	<u>L5</u>
<u>L4</u>	L2 and integrating plasmid	82646	<u>L4</u>
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<u>L1</u>	shiuan.in.	76	<u>L1</u>

END OF SEARCH HISTORY

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Search Results - Record(s) 1 through 3 of 3 returned.

1. Document ID: US 20030104584 A1

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L3: Entry 1 of 3

File: PGPB

Jun 5, 2003

PGPUB-DOCUMENT-NUMBER: 20030104584

PGPUB-FILING-TYPE: new

DOCUMENT-IDENTIFIER: US 20030104584 A1

TITLE: Yeast with high biotin-productivity and the preparation method thereof

PUBLICATION-DATE: June 5, 2003

INVENTOR-INFORMATION:

NAME CITY STATE COUNTRY RULE-47

Shiuan, David Kaohsiung TW

US-CL-CURRENT: 435/119; 435/254.2, 435/320.1, 435/483

Full Title Citation	Front Review	Classitication Date	Reference	Sequences	Attachments	Claims	KANC	Draw Desc Ima
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2. Document ID: US 20030003549 A1

L3: Entry 2 of 3 File: PGPB Jan 2, 2003

PGPUB-DOCUMENT-NUMBER: 20030003549

PGPUB-FILING-TYPE: new

DOCUMENT-IDENTIFIER: US 20030003549 A1

TITLE: DETECTION OF HUMAN HEPATITIS B VIRUS SURFACE ANTIGEN MUTANTS BY SPECIFIC

AMPLIFICATION AND ITS APPLICATION ON GENE CHIP

PUBLICATION-DATE: January 2, 2003

INVENTOR-INFORMATION:

NAME CITY STATE COUNTRY RULE-47 OON, CHONG-JIN SINGAPORE SG CHEN, WEI-NING SINGAPORE SG LEONG, AI-LIN SINGAPORE SG KOH, SHIUAN SINGAPORE SG

US-CL-CURRENT: <u>435/110</u>

Full Title Citation	Date Reference Sequences		KWIC Draw Desc Ima
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3. Document ID: US 6759193 B2

L3: Entry 3 of 3 File: USPT Jul 6, 2004

US-PAT-NO: 6759193

DOCUMENT-IDENTIFIER: US 6759193 B2

TITLE: Detection of human hepatitis B virus surface antigen mutants by specific

amplification and its application on gene chip

DATE-ISSUED: July 6, 2004

INVENTOR-INFORMATION:

NAME CITY STATE ZIP CODE COUNTRY Oon; Chong-Jin Singapore SG Chen; Wei-Ning Singapore SG Leong; Ai-Lin Singapore SG Koh; Shiuan Singapore SG

US-CL-CURRENT: 435/6; 435/5, 435/91.2, 536/23.72, 536/24.3, 536/24.33

Full Title Citation Front Review Classifica	ation Date Reference	Claims KV0C Draw, Desc Ima
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Hong Y.R. and Shiuan, D.
Direct Submission
Submitted (16-DEC-1999) Graduate Institute of Biochemistry,
100, Shih-Chuan 1st Road, Kaohsiung, Taiwan
Location/Qualifiers
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AL022245 S.pombe c
AL031764 S.pombe c
AL402619 T3 end of
AR075303 Sequence
166541 Sequence
AR306523 Sequence
X63612 S.cerevisia
AJ224930 Schizosac
AK101236 Oryza sat
AK059296 Oryza sat
CQ805820 Sequence
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X94332 S.cerevisia
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X72701 S.cerevisia
                                                                              September 17, 2005, 13:24:44; Search time 5408 Seconds (without alignments) 10644.378 Million cell updates/sec
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Copyright (c) 1993 - 2005
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CKYCAQSSRUDTGLKAEKWYKVDEVIKEAEBAKRNGSTRFCLGAAWRDWKGRKSAMKR
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GTPMAEELADPKSKKLQFDEILRTIATARIVMPKAIIRLAGRYTMKETEQFVCFWAG
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VII reading frame ORF YGR286c.
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Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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Submitted (14-MX-1996) Data collected by MIPS on behalf of the
Submitted (14-MX-1996) Data collected by MIPS at the
Buropean yeast chromosome VII sequencing project. MIPS at the
Max-Planck-Institut fuer Biochemie, Am Klopferspitz 18a D-82152
Martinsried, FRG; E-mail: Mewes@mips.embnet.org
Location/Qualifiers
                                                                                       4815 GTTAAGAACAAGCAAGTTGAAGTTGATGAGATTGTCAGAACCATTGCTACTGCAAGATTG
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                       4695 GGTGAGACCCAAAGAGGACCGTGTATCTTTCCTCTACACCTTGGCCACAATGGATCAGCAT
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GGTGAGACCCAAGAGGACCGTGTATCTTTCCTCTACACCTTGGCCACAATGGATCAGCAT
                                                                    CCAGAGICTCTTCCAATCAACAGACTGGTCCCAATCAAGGGCACGCCAATGIATGAAGAA
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/db_xref="taxon:4932"
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complement (660. .1787)
/gene="BIO2"
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S.cerevisiae chromosome
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Voet, M. and Volckaert, G.
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BAAKBAKANGSTRFCMGAAWREMKGRKSNLKKIKWITAVHDLGMESVTLGMVDKD
ATELKSAGLTAYNHIIDTKEHYPKVISTRSFDDRLKTFKNVGSGLKACTGGILGLG
ETQEDRVSFLYTLATHDOPPESLPINRLVPIKGTPMYEBVKNKQVSVDBIVRTIATAR
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Conservative 0; Mismatches 0;
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'gene="Bio2"
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                                                                                                   PLN 14-APR-1997
                                                                                                                                                                                                                                                                                               Volckaert,G., Voet,M. and Robben,J.
Sequence analysis of a near-subtelomeric 35.4 kb DNA segment on the Sequence analysis of a near-subtelomeric 35.4 kb DNA segment or the right arm of chromosome VII from Saccharomyces cerevisiae carrying the MALI locus reveals IS complete open reading frames, including ZUOI, BGL2 and BIO2 genes and an ABC transporter gene 774sest 13 (3), 251-259 (1997)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Volckaert,G.
Volckaert,G.
Direct Submission
Submitted (14-DEC-1995) G. Volckaert, Laboratory of Gene
Technology, Catholic University of Leuven, Willem de Croylaan 42,
B-3001 Leuven, BELGIUM
Location/Qualifiers
                                                                                                                                                                                                                                         Eukaryota, Fungi, Ascomycota, Saccharomycotina, Saccharomycetes,
Saccharomycetales, Saccharomycetaceae, Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15763 AATATGCATTGTCTTTAGATGAACCAAGTCATTGGTGGACAAAATCGCAATTAAAAGAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /map="right arm"
/clone="cosmid pEGH452"
/clone_lib="H.Tettelin (Louvain-la-Neuve, Belgium)"
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  AATGGGGATTGCAACCTATGGAGGCATTTAAGTACGA 670
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Pred. No. 1.4e-128;
0; Mismatches 281;
                                                                                                                                                                                                    cerevisiae (baker's yeast)
                                                                                                 JCHVIIRA 35400 bp cerevisiae DNA for fragment from
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/mol_type="genomic_DNA"
/strain="FY1679"
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/chromosome="VII"
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                                                           Length 4068;
  CNS I FTGKKML TTMCNGWDEDKAMLAKWGLQPMEAFKYDRS
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                                                         Score 519.4; DB 8;
Pred. No. 1.5e-128;
0; Mismatches 281;
                                                       Query Match 43.7%;
Best Local Similarity 70.9%;
Matches 707; Conservative
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I (bases I to 1847)
Zhang, S., Sanyal, I., Bulboaca, G.H., Rich, A. and Flint, D.H.
The gene for biotin synthase from Saccharomyces cerevisiae:
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Zheng, S.
Zheng, S.
Direct Submission
Submitted (12-MAR-1993) S. Zheng, 16-739 Dept. of
Massachusetts Institute of Technology, Cambridge,
Location/Qualifiers
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Arch. Biochem. Biophys. 309 (1), 29-35 (1994)
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/db_xref="G1:288357"
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/strain="20B-12"
/db_xref="taxon:4932"
/chromosome="VII"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTATCCAAAGGTTATTTCAACTAGAAGTTACGATGAGAGGTTGCAAACAATCAGGAATGT
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                                                                                                                          CR382134
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                                                                                                                          CR382134 Accession
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 451.6; DB 8;
Pred. No. 2.4e-110;
0; Mismatches 339;
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Best Local Similarity
Matches 696; Conserv
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                                                                RESULT 7
CR382134 04/c
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                                                                                                                                                                                                                                                                          ACCAACTGGACCAGAGATGAGGTGTCCAAAATCTACAACATGCCTTTGATGGATCTTGTT 84258
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                                                                                                                                                                                                                                                                                                                                                                                                                         <u> Argaagggregaaagaacgccraaagaacgreaagagargargargcrecrecagga</u>
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                                                                                                                                                                                                                                                                                                                  CACTATGCTCAGGTGCAACACAGAAGGTTCCAACAACTTCAGAGGTTCAATTGTGCACT
                                                                                                                                                                                                                                                                                                                                                         84259 Trcaaggccgccaccgrccaccaccaccaccaccaccacccrccagaggrccacrr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGATÁCACTÁCTGGTGTTGÁGGCGGGGAGGCAGCTGAGCCAGGTGAGGTTATTGCCGCT
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                                                                                                                                                                                            Gaps
                                                                                                                                               Length 110000
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                                                                                                                                                                                          Indels
                                                                                                                                               Score 458.8; DB 8;
Pred. No. 2.8e-112;
0; Mismatches 297;
                                                                                                                                                 18.6%;
al Similarity 68.3%;
653; Conservative
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      CR382130_33
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inuation (19 c
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                                                                                                                                                    Query Match
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954 ATTAGTTCCAATCCAGGTACTCCAATTGTTGAAGTGTTGAAAAATGCCCCAAAGGAAG 1013
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Wood, V., Gwilliam, R., Rajandream, M.A., Lyne, M., Lyne, R.,
Stewart, A., Sgouros, J., Peat, N., Hayles, J., Baker, S., Basham, D.,
Bowman, S., Brooks, K., Brown, D., Brown, S., Chillingworth, T.,
Churcher, C., Collins, M., Connor, R., Cronin, A., Hadiln, N., Harris, D.,
Hadalo, J., Hodgson, G., Goble, A., Hadlin, N., Harris, D.,
Huckle, B.J., Hunt, S., Jagels, K., James, K., Jones, L., Jones, M.,
Leather, S., McDonald, S., McLean, J., Mooney, P., Moule, S.,
Mungall, K., Murphy, L., Niblett, D., Odell, C., Oliver, K., O'Neil, S.,
Bearson, D., Quall, M.A., Rabbinowitech, E., Rutherford, K., Rutter, S.,
Saunders, D., Seeger, K., Sharp, S., Skelton, J., Simmonds, M.,
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   AGGTAGAAAGTCAAACTTGAAGAAAATCAAAGAGATGATCACTGCTGCTGCATGAC---CT
                              AGGAAGAAAGTCTGCCTTAGACAAAATCAGTAAAGTTGTTAAACAAATCAACGAGTT
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                                                                                                           GAAGTTGGAAACTTGTGTTACTCTCGGGATGATCAACGAAAAGCAGGCTGAAATTTTAAA
                                                                                                                                                                                    714 ACAGAATGGTTTGACTGCCTACAACCACACATTGACACTTCAAGAGAACATTATCCAAA
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Weinstock, K.G. and Bush, D.
Nucleic acid sequences relating to Candida albicans for diagnostics
and therapeutics
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/gene="ark1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequencing project, Sanger Institute, The Wellcome Trust Genome Campus, Hinkton, Cambridge CB10 1SA, E-mail: pombe@sanger.ac.uk and AGOWA GmbH, Glienicker Weg 185, D-12489 Berlin, Germany On Apr 14, 1999 this sequence version replaced gi:2995362.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Details of S. pombe sequencing at the Sanger Institute are available on the World Wide Web.

(WRL, http://www.ganedb.org/genedb/pombe/index.jsp) (URL, http://www.sanger.ac.uk/Projects/S_pombe/)
CDS are numbered using the following system eg SPAC5H10.01c. SP (S. pombe), A (chromosome 1), c5H10 (coemid name), .01 (first CDS), c (complementary strand). However, clones may have been reorientated since the original submission, therefore the complementary strand notation may be invalid for strand inference. IMPORTANT: This sequence MAY NOT be the entire insert of the sequenced clone. It may be shorter because we only sequence overlapping sections once. Location/Qualifiers
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/note="nominal overlap with cosmid SPCC330, EM:AL031603 S.
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evidence=ISS; db_xref=GOC:unpublished; with=SPTR:P05792;
date=20030609
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biosynthemis; GOid=GO:0009082; evidence=ISS;
db_xref=GOC:unpublished, with=SPTR:; date=20030609
aspect=F; term=threonine dehydratase activity;
GOid=GO:0004794; evidence=ISS; db_xref=GOC:unpublished;
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complement (709. .1680)
/gene="SPCC320.14"
/BC_number="4.3.1.19"
/note="threonine dehydratase (predicted); involved in
threonine catabolism; involved in branched chain amino
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/note="rpl242 see c330 for full length CDS"
copel=mrpl242 see c330 for full length CDS"
/gene="spcc320.14"
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/organism="Schizosaccharomyces pombe"
/mol_type="genomic DNA"
/strain="972h-"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:4896"
/chromosome="III"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'clone="cosmid c320"
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FEATURES

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//Jecus. distrine/threonine protein kinase; aurora homolog; involved in spindle checkpoint; involved in spindle formation (required) (PMID 1192803); involved in siter chromatid separation (required) (PMID 11950927); involved in the microtubule attachment response (required) (PMID 11950927); involved in the microtubule attachment response (required) (PMID 1186091); interacts physically and/or genetically with the inner centromere protein Piclp (PMID 11950927); interacts physically and/or genetically with the inner centromere protein Birlp (PMID 11950927); interacts physically mid-or genetically with survivin (PMID 11950927); involved in protein amino acid phosphorylation (EERIO Of Hht3p) (PMID 11792803); similar to S. cerevisiae
                                                                                                                                                          /procein_id="CAA18316.1"
/db_xref="G1:2995376"
/db_xref="G0A:0599376"
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/db_xref="UniProch5wigs-Proci:059791"
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/db_xref="UniProch5wigs-Proci:059791"
/db_xref="UniProch5wigs-Proci:059791"
/d
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LLGIGOESIKASDFGWSVHABSRRRTTLGGTLDYLPPENVEGKEHTEKVDLWSLGYLTY
EFLYGAPPFEDMSGHSATYKRIAKVDLKIPSFVPPDARDLISRLLQHNFEKRMSLEQY
MRHPWIVKYKOSWTRKSSESS"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'note="Pfam match to entry S_T_dehydratase ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          08.01.3003 trimmed to 2nd met PMID 12676091"
component unknown;
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tRNA Glu anticodon CTC, Cove score 74.15"
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/note="8ynonym: SPCC330.17c"
complement(join(4707. .4714,4781. .5330))
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complement (join (4707. .4714,4781.
aspect=C; term=cellular compone
GOid=GO:0008372; date=20030609"
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/gene="SPCC320.14"
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prot ein kinase domain"
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/gene="SPCTRNAGLU.09"
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/gene="SPCTRNAGLU.09"
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Schizosaccharomycecares; Schizosaccharomyceaceae; Schizosaccharomyces.

Schizosaccharomyces.

I (bases 1 to 4088)

Wood, V. Gwilliam, R., Teath, N., Hayles, J., Baker, S., Basham, D., Brown, S., Chilliam, R., Brown, D., Brown, S., Chilliam, D., Bowman, S., Brooks, K., Brown, D., Brown, S., Chilliam, Davis, P., Churcher, C., Collins, M., Connor, R., Cronin, A., Hamlin, N., Harris, D., Hidalgo, J., Hodgson, G., Holroyd, S., Hornsby, T., Howarth, S., Huckle, E.J., Huhrt, S., Jagels, K., James, L., Jones, M., Leather, S., McDonald, S., McDent, D., Odell, C., Oliver, K., Oliver, K., Oliver, K., Saunders, D., Quall, M.A., Rabbinowitsch, E., Rutherford, K., Rutter, S., Saunders, D., Seeger, K., Sharp, S., Skelton, J., Simmonds, M., Squares, S., Stevens, K., Taylor, K., Taylor, R., Taylor, R., Walsh, S., Marren, T., Whitehead, S., Woodward, J., Volckaert, G., Malsh, S., Marren, T., Whitehead, S., Woodward, J., Volckaert, G., Malsh, S., Marren, T., Whitehead, S., Woodward, J., Volckaert, G., Dager, M., Schafer, M., Muller-Auer, S., Gabel, C., Hilbett, H., Borzym, K., Langer, P., Zimmermann, W., Wedler, H., Weither, R., Purnelle, B., Goffeau, A., Caker, M., Gaillarth, C., Hurst, S., Lelaure, V., Mottier, S., Gallbert, R., Purnelle, B., Goffeau, A., Cateke, M., Gaillarth, C., Jimmert, S., Lelaure, V., Mottier, S., Cruzado, L., Gruzado, L., Jimmer, J., Sanchez, M., Mocone, K., Hurst, S.M., Lucas, M., Rochet, M., Sanchez, M., Benito, J., Dominguez, A., Lewer, T., McComble, W.R., Paulsen, I., Potashkin, J., Shpakovski, G.V., Lowe, T., McComble, W.R., Paulsen, I., Potashkin, J., Shpakovski, G.V., The genome sequence of Schizosaccharomyces pombe
                                                                                                                                                                                                                                                                                                                                                                                   39164 CTTTTGGTCCCGAPTCCTGGCACCCTGT---AGGAGACGCTGTAAAAGAGAGACTTCCG 39220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            39221 ATTCATCCTTTCCTTCGCTCCATTGCAACAGCTCGTATTTGCATGCCAAAGACTATCATT 39280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      39341 GGTGCTAATGCAGTTTTTACCGGTGAAAAATGCTTACTACTCCTGCTGTTCTTGGGAC 39400
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                                                                        39044 ccrecerreaacerrreragecerreerarrrragereragecaacaaaaacearear
                                                                                                                                                         802 GTATCTTTCCTCTACACCTTGGCCACAATGGATCAGCATCCAGAGTCTCTTCCAATCAAC
                                                                                                                                                                                                                                                                                                              GITGATGAGATTGTCAGAACCATTGCTACTGCAAGATTGGTCATGCCAACGTCTATTATC
742 TCTGGATTAAAGGCATGCACAGGTGGTATTCTTGGTCTTGGTGAGACCCAAGAGGACCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             982 AGATTGGCTGCAGGAAGATATACAATGAAAGAGGCAGAACAGGTGATGTGCTTCATGGCT
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Schizosaccharomycetales, Schizosaccharomycetaceae,
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Schizosaccharomyces pombe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      38684 CGCTACAATACCGGTGTCAAGGCCACTAAGCTCATGAAATTGACGAAGTTTTGGAAAAG 38743
                                                                                                                                             /protein id="CAA18314.1"
/db_xref="G1:2995374"
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/translation="MSEDPQSWSKERKOKERVKRALMSQSPVIFLKTALDRLNCNIE
AKDISCOPCOAQSTGGYIPGKGIYLCENRLYTKKMAENTIAHEMIHMEDDHREEVDWN
NLRHQACSEIRASSMSGECRWTKELRFGNIKTFRKHHQECVKRRATISVQGNPNCKSK
EQABAIVEEVENSCRNDFRPFEKIY"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       38564 TTTAGAGCCGCTTCCATACATAGAAAATTCCACGACCCCAAGAAAGTTCAACAATGCACT 38623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               38744 GCTAAAATTGCAAAGGCTAAAGGAAGCACTAGATTTTGTATGGGAAGTGCCTGGCGTGAT 38803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     38804 TTGAATGGTCGCAATCGCACCTTTAAAAATATTTTGGAAATCATCAAAGGTTCGCAGC 38863
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      38864 ATGGATATGGAAGTTTGCGTAACCCTTGGTATGTTAAATGAACAGCAAGCCAAGGAACTA 38923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     38984 AAGATTATCAGCACTAAGGACATATGATGAACGGTTAAATACTATTGACAATCTTCGGAAA 39043
                        note="neutral zinc metallopeptidase (predicted); similar o S. cerevisiae YNR020C"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         262 CACTATGCTCAGGTGCAACACAGAAGGTTCCAACAACCTTCAGAGGTTCAATTGTGCACT 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTTATGAATATCAAAACTGGTGGTTGTACCGAGGACTGTAAGTACTGTGCCCAATCACAG 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CGTTACAACACTGGTGTCAAGGCTGAAAGAATCATCCAAGTTGATGAGGTGATTGAAGCT 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      442 GCAAAGGAGGCAAAGGCCAATGGATCTACAAGGTTCTGTATGGGTGCTGCTTGGAGAGAG 501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        502 ATGAAAGGTAGAAAGTCAAACTTGAAGAAAATCAAAGAGATGATCACTGCTGTCCATGAC 561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTTGGAATGGAGAGTTGTGTCACCCTGGGAATGGTTGATAAAGACCAAGCCACTGAATTG 621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAAAGTGCTGGGTTGACGGCGTACAACCATAACATTGATACTTACAAGGAACACTATCCA 681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAGGTGATCTCCACAAGAAGCTTTGATAGATTGAAAACATTCAAAAAGGTTCAAGGA 741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement (4775. .4780)
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/note="gerC320.12"
/gene="SPCG320.12"
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/note="SPCG320.12"
join(5867. .5922,6076. .6162,6325. .6724)
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/note="SPCG320.11c"
/note="SPCG320.11c"
/gene="SPCG320.11c"
/gene="SPCG320.11c"
/gene="SPCG320.11c"
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                                                                                                                                                                                                                                                                                                                                                                                                                       complement(4715. .4738)
/gene="SPCC320.12"
/note="ctaactattcattctttcgtctag, splice branch and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="GOA:059788"
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/db_xref="GI:2995373"
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PLN 20-JUN-2003

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NSGNYNNNNSGNNNQOHQQSSSSLQCLASSFLNSSSGNSNKQNYNNNNNQNYGNNNNQ
NYNNNNNSSQGGNSQGGSGLLGQAVNMFLKS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tränslation="mptrtirqqirrssalslvrnnwtreeiqkiydtplidlifraa
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DRVGLIHSLATMPTHPESVPFNLLVPIPGTPVGDAVKERLPIHPFLRSIATARICMPK
TIIRPAAGRNTCSESEQALAFMAGANAVFTGEKMLTTPAVSWDSDSQLFYNWGLEGMQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="UniProt/Trembl:059779"
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                                                                                                                                                 Details of S. pombe sequencing at the Sanger Institute are available on the World Wide Web.

(URL, http://www.genedb.org/genedb/pombe/index.jsp) (URL,

thtp://www.sanger.ac.uk/Projects/S_pombe/)

CDS are numbered using the following system eg SPACSH10.01c. SP (S. pombe). A (chromosome 1), c5H10 (cosmid name), ol (first CDS), c (complementary strand). However, clones may have been reorientated since the original submission, therefore the complementary strand notation may be invalid for strand inference. IMPORTANT: This sequence MAY NOT be the entire insert of the sequenced clone. It may be shorter because we only sequence overlapping sections once. Location/Qualifiers

    .2935
'note="nominal overlap with cosmid SPCC320, EM:AL022245 S.

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                            Direct Submission
Submitted (28-SEP-1998) European Schizosaccharomyces genome
sequencing project, Sanger Institute, The Wellcome Trust Genome
Campus, Hinxton, Cambridge CB10 1SA, E-mail: pombe@sanger.ac.uk
Rajandream, M.A., Barrell, B.G., Murphy, L. and Harris, D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /_octe="synonyms: SPCC1235.02, SPCC320.01c"
1374. .2465
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            organism="Schizosaccharomyces pombe"
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|strain="972h-"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      xref="UniProt/Swiss-Prot:059778"
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/chromosome="III"
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/gene="SPCC1235.03"
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'qene="SPCC1235.03"
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     AUTHORS
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Ardtelslktttdvilcsnyknalwilciiketohnemsnyklssotakkossator
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FVDREQGSKRRINIISTSLPWRESPCKFLEHHUIGALLIGIRRLDFHGLHIAFBYDB
KGWPKFMRIQPILDMSYTBIWDLLLETNTKYCSLYDRGYTSLGGVSDTSPNPALKNPD
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TOGRSRSSANDYTTPPVNNTLLTPPRAPPEDPUTTSSPATTSPYNDAITRSYVPOADI
HQYINTLAOTKWDETAALSILSQKXLSCDLGIPIQEHKRFKQSPVASNMFTVGGSNR
VQSQKRSIRDKYIQMPNDSTQASLMPSYTRKTSNASKKLITEEDEFYDSEEFPALYH
KDTSALLERTVLNFINSSTAKELSDTACCPLSHSKLLLLEHRPFOTLAAGATIKHPDVP
SKPGRRGRRRENDAYGXIVANGETWRGYYAIDNILAKCEFLGNTSKGRASKGIKK
EMSNGELNIVUMRSVPTRAADNSDFPKFVTEQPKTLLASDVQLKSYQLVGVNWLHILYQ
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|Trainlat.ton="MLPYNAYLSDNOFKRKESDENPQSEVYGSGQTGLPSSYGNPQSY
|Trainlat.ton="MLPYNAYLSDNOFKRESDNOFMTDYSGTSSYASTPMSNAYSRDAPAA
|TrepVQQSSAAYGGVNNSMGGGAYTTSENTQFNATDYSGTSSYASTPMSNAYSRDAPAA
|INNNFGYSYVGQSSQPVPSYNPLPSYNTASLPNAGIPAAMPGMPSGYFGTVPIPQGGY
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LFRKFYDDEKLKQMAKDIMQEBQYKNANBQYIYEDMEVMSDFELHRLCRSFPTLQSYT
LKDDPWNDSGKIRVLKELLPKMKEBGSRILLFSQFTQMLDILEQVLDTLKISYVRLDG
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                                                                                                                                                                                                                                                                                                                                                   /gene="SPCC1235.03"
/note="mRNA from SPD171"
complement(join(5485. .5736,5785. .6193,6247. .6383))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="crarcgtttattacaag, splice branch and acceptor" complement(6241. .6246)
/gene="SPCC1235.04c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .6193,6247. .6383))
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/note="DEAD/DEAH box helicase; SNF2 family; helicase
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complement (5737. .5747)
/gene="SPCC1235.04c"
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complement(5779. .5784)
/gene="SPCC1235.04c"
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complement(7185. .11294)
/gene="SPCC1235.05c"
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/gene="SPCC1235.05c"
/note="mRNA from AU013698"
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/db xref="G1:3668152"
/db xref="GOA:074842"
/db xref="UniProt/TrEMBL:
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/gene="SPCC1235.04c"
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/gene="SPCC1235.04c"
/EC_number="2.7.7.2"
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/clone="AT0AA003D06"
/clone_lib="AT0AA"
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MLDEHNGNNTKPFITGNESDGFFKVSSNNNSKQTDAEFINTGVPLEGSQPNSVEKTD
LADGDEKANITKTEMKESTVCGNNKELRETMKGENVQTDSNAAVPSSKSSTEEPNESVL
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                                                                                         complement (8184. .8435)
/gene="SPCC1235.05c"
/note="Match to helicase_C , Score 83.11"
complement (8721. .9638)
/gene="SPCC1235.05c"
/note="Match to SNF2_N , Score 344.47"
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Direct Submission

Submitted (07-SBP-2000) Genoscope - Centre National de Sequencage,

Submitted (07-SBP-2000) Genoscope - Centre National de Sequencage,

Submitted (07-SBP-2000) Genoscope - Centre National de Sequencage,

This STS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces servazii, Zygosaccharomyces rouxii,

Saccharomyces Rluyveromyces thermotolerans, Rluyveromyces saccharomyces servazii, Zygosaccharomyces rouxii,

Saccharomyces kluyveri, Kluyveromyces thermotolerans, Rluyveromyces lactis var. lactis, Rluyveromyces marxianus var. marxianus, Pichia angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila, Candida tropicalis and Yarromia lipolytica. Genomic inserts of 3 to keywords for description of this sequence and for the sequence of the other extremity of this insert.
GGTTGTAATGCCATCTTCACAGGTAAGAAATGCTCACAACAATGTGTAACGGCTGGGAT 1101
                                                                                  2271 GGTGCTAATGCAGTTTTTACCGGTGAAAAAAGCTTACTACTCCTGCTGTTTTCTTGGGAC 2330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                CNSO6K9X 847 bp DNA linear STS 10-JAN-2001 T3 end of clone ATOAA003D06 of library ATOAA from strain CBS 4311 of Saccharomyces servazzii, sequence tagged site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Souciet, J.L., Aigle, M., Artiguenave, F., Blandin, G., Bolotin-Fukuhara, M., Bon, E., Brottier, P., Casaregola, S., Bolotin-Fukuhara, M., Bon, E., Brottier, P., Casaregola, S., Bolotin-Fukuhara, M., Dujon, B., Durrens, P., Lapingle, A., Llorente, B., Malpertuy, A., Neuvegliae, C., Ozier-Kalogeropoulos, O., Porier, Saurin, W., Tekaia, P., Toffano-Nioche, C., Wesolowski-Louvel, M., Wincker, P. and Weissenbach, J. Genomic exploration of the hemiascomycetous yeasts: 1. A set of yeast species for molecular evolution studies
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                                                                                                                                                                                                                     complement(<8. .>847)
/note="similar to Saccharomyces cerevisiae ORF YGR286c
BIO2 ; biotin synthetase ]"
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                                                                                                                                                                     1102 GAGGATAAAGCCATGTTGGCTAAATGGGGTCTGAAACCAATGGAGAGTTTCAAATA
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Saccharomyces servazzii
Bukaryota; Fungi; Ascomycota; Saccharomycotina; Sacch
Saccharomycetales; Saccharomycetaceae; Saccharomyces
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/mol_type="genomic DNA"
/strain="CBS 4311"
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Holmes, T., Zhang, S., Rich, A., DiPersio, C.Michael. and Lockshin, C. Stable macroscopic membranes formed by self-assembly of amphiphilic peptides and uses therefore peptides and uses therefore Patent: Location/Qualifiers
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Unclassified.
2 Anses 1 to 3083)
Zhang, S., Lockshin, C., Rich, A. and Holmes, T.
                                                                                                                                                                                                                                                                       Query Match 27.6%; Score 328.2; DB 6; Best Local Similarity 72.1%; Pred. No. 4.3e-77; Matches 445; Conservative 0; Mismatches 163;
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/organism="unknown"

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Stable macroscopic membranes formed by self-assembly of amphiphilic peptides and uses therefor Patent: US 5670483-A 1 23-SEP-1997;
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Zhang, S., Lockshin, C., Rich, A. and Holmes, T.
Stable macroscopic membranes formed by self-assembly of amphiphilic
peptides and uses therefor Pare 2003;
Patent: US 6548630-A 1 15-APR-2003;
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/organism="unknown"
/mol_type="unassigned DNA"
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1 (bases 1 to 3083)
Zhang,S., Lockshin,C., Herbert,A., Winter,E. and Rich,A.
Zuotin, a putative Z-DNA binding protein in Saccharomyces
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                                                                                                                   Length 3083;
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Saccharomyces cerevisiae (baker's yeast)
Saccharomyces cerevisiae
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S.cerevisiae ZUO1 gene for zuotin.
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/translation="VTKILPRRKLINNSMLSGTDLTPGEPLSSWTKMSQWTLLTETTSV
TLKERTRPQETRRLLITLDWSNLLKELSVKI PVSKCSKKKRRRKREEBNGKEKPVPE
LKLKLRPRPKLKRRLKLNLKPRLTPPQKLTKRRLRRPRKTREPSVTLLRKLTT
LVMLTRPPRLTNKLV"
2746. . 2754
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GLSKLRFRATESQI IKAHRKQVVKYHPDKQSAAGGSLDQDGFFKI IQKAFETLTDSNK
RAQYDSCDFYADVPPPKKGTDYDFYBARGNFREARFSKKTFT IFSLGNKDSSKKEVB
QYAFWHIF PSGWT FFFILDEDVPDDSSNRDHKRY I ERKNKAARDKKKTADNARLVKLV
ERAYSEDRE IKMFKEEEKKETERKWEREAGRAAEABAKAKABABAKKAAESBAKAN
SAKADKKKAKERAAKKKNKRAIRNSAKEADY FGDADKATTIDEQVGLIVDSLNDEE
LVSTADKI KANAAGAKKUKRAIRNSAKEADY FGDADKATTIDEQVGLIVDSLNDEE
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2 (bases 1 to year)
Zhang,S.
Direct Submission
Direct Submission
Submitted (20-DEC-1991) S. Zhang, Massachussetts Inst of
Submitted (20-DEC-1991) S. Zhang, Massachussetts Inst of
Technology, 16-739 Dept of Biology, M I T, Cambridge MA 02139, USA
Technology, 16-739 Dept of Biology, M I T, Cambridge MA 02139, USA
Technology, 16-739 Dept of Biology, M I T, Cambridge MA 02139, USA
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chromosome="VII"
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The present invention relates to a yeast with high biotin-productivity and a method for its preparation. The yeast is transformed by an integrated plasmid, which includes the edible yeast (Candida utilis) biotin synthase gene, an assistant DNA sequence for the integration of the plasmid into a host genome, a promoter sequence, and a selection marker. The prepared yeast with high biotin-productivity or recovered biotin is useful as feed additives, food additives or cosmetics. The present sequence represents C. utilis biotin synthase gene.

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ALIGNMENTS

Yeast, high biotin-productivity, edible yeast, biotin synthase gene, feed additive, food additive, cosmetic, gene, ds. New integrated plasmid, useful for preparing yeast with high biotin-productivity used as feed additives, food additives or cosmetics. Candida utilis biotin synthase gene. ВЪ. Claim 3; Page 3; 20pp; English. ADA09588 standard; DNA; 1188 02-JAN-2001; 2001US-00752957. 07-OCT-2000; 2000TW-00120972. (first entry) WPI; 2003-567956/53 (SHIU/) SHIUAN D. US2003104584-A1. Pichia jadinii. 05-JUN-2003. 06-NOV-2003 ADA09588; Shiuan D;

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Diploid fungal cell; allele; gene disruption cassette; promoter replacement fragment; antifungal; fungicide; gene therapy; infection; Candida albicans; gene; ds.
                                                                                                                                                                                                                    C. albicans specific gene, orf6.4105, DNA
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1081 ACAATGTGTAACGGCTGGGATGAGGATAAAGCCATGTTGGCTAAATGGGGTCTGAAACCA
                                                                                                                                                                                                                   1141 ATGGAGAGTTTCAAATACAAACCAAGGGAGGTTGCATTCGGTGCTTGA 1188
                                                                                                                                                                                                                                                                               1141 ArgeAGAGTTTCAAATACAAACCAAGGGAGGTTGCATTCGGTGCTTGA 1188
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Constructing a strain of diploid fungal cells in which both alleles of a gene are modified comprises modifying the alleles of a gene in the fungal cells by recombination using a gene disruption cassette and a promoter

The invention relates to a novel method for constructing a strain of diploid fungal cells in which both alleles of a gene are modified. The method comprises modifying the alleles of a gene in diploid fungal cells method comprises modified. The recombination using a gene disruption cassette and a promoter coplaction of diploid fungal cells each of which comprises modified alleles of a different gene; a strain of diploid fungal cells comprises modified alleles of a gene, where the first allele of the gene is modified alleles of a gene, where the first allele of the gene is required by a gene disruption cassette comprising a nucleotide sequence encoding an expressible selectable marker; and the expression of the second allele of the gene is regulated by a heterologous promoter the second allele of the gene is regulated by a heterologous promoter that is operably linked to the coding region of the second allele of the gene encodes the polypeptide mentioned above; a collection of diploid fungal strains comprising the diploid strains cited above, where substantially all the different genes that encode the above amino acid sequences are modified and are present in different diploid arrains in the collection; a nucleic acid molecule microarray comprising nucleic acid molecules, where each nucleic acid molecule comprising comprising any of the 310 nucleotide sequences listed in the comprising any of the 310 nucleotide sequences listed in the

us-09-752-957f-1.rng

correctionation (ADP98816-ADP98825); identifying a gene that is essential to the treatstance of a diploid fungus, or that contributes to the resistance and/or pathogenicity of a fungus, or that contributes to the resistance of a diploid fungus to an antifungal agent; identifying an antifungal agent that inhibition of growth of a diploid fungus, or a therapeutic agent that inhibits the growth of a diploid fungus, or a therapeutic agent that inhibits the growth of a diploid fungal cell; a purified or isolated muclaic consists of any of the above-mentioned ablicans, where the gene product consists of any of the above-mentioned ablicans, where the gene product consists of any of the above-mentioned ablicans, where the gene product consists of any of the above-mentioned amino acid sequences; a vector comprising a promoter operably liked to the nucles cade molecule cited above: a host cell containing the vector; a purified or isolated polypeptide comprising any of the 61 amino acid sequences given in the specification (App97718-App9778); a fusion protein comprising a fragment of a first polypeptide comprising any of the flast compound which modulates the above: a host cell control of a polypeptide comprising any of the polypeptide comprising any of the polypeptide comprising any of the polypeptide comprising any of App9816-App9825; a first allele of agen comprising any of App9816-App9825. A producing a percent of a second allele of the gene of any of App9816-App9825; a first allele of agen comprising any of App9816-App9825; a first allele of agen comprising or the control of a percentoged by a nucleic acid comprising any of App9816-App9825; a first allele of a gene comprising prowth or proliferation of Candida ablicans; a pharmaceutical modern of a subject by Candida albicans; a pharmaceutical composition and antimycotic compound; a condain ablicans; a pharmaceutical composition and any of App9816-App98825. In a pharmaceutical and a process and a process and a process and a process and any of App98816-App98825. The n useful for identification and validation of gene products as effective targets for therapeutic intervention, for identifying and validating gene products as effective targets for therapeutic intervention, and for collecting identified essential genes. This polynucleotide sequence represents a Candida albicans fungal specific gene of the invention. provided on the WIPO website.

18; 35.2%; Score 417.6; DB 12; Length 67.0%; Pred. No. 6.7e-113; ive 0; Mismatches 299; Indels 0, Conservative Similarity 645; Query Match Local

Sequence 1125 BP; 362 A; 218 C; 242 G; 303 T; 0 U; 0 Other;

CTGGACCAAAGAAGAAATTAAAGCTATATATGACACACCACTCATGGACTTGATGCACTA 266 TGCTCAGGTGCAACACAGGTTCCAACAACCTTCAGAGGTTCAATTGTGCACTCTTAT 326 CTGGACCAAAGATGAAATTAGCAAAATTTACAATGCTCCATTGATGGATTTGATTTTCAA 218 CGCTCAATTGAAACATCGTGAGTACCAAAAACCTGCTGAAGTCCAATTATGTACTCTTGT 278 GAATATCAAAACTGGTGGTTGTACCGAGGACTGTAAGTACTGTGCCCAATCACAGCGTTA 386 TAACATTAAGCAGGGTGGATGTACCGAAAACTGTTCTTACTGTTCTCAATCATCGAAACA 338 279 159 267 219 207 Best Loca Matches

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1031 1055 1151 1115 635 743 863 911 875 339 rgaracregaerrcaaecreaaaa---cresacrregarecrerearesacarrecrae 395 396 AGATGCGAAAGCACGAGGTGCTACTAGAGTTTGCCTTTGGTTCCGCTTGGAGAGATATGCA 455 563 515 623 575 803 755 387 CAACACTGGTGTCAAGGCTGAAAGAATCATCCAAGTTGATGAGGTGATTGAAGCTGCAAA 996 TITCATGAGTGGGGTCAATGCTATTTCACCGGTAAGAGAATGTTGACTACAATGTGTAAA 456 AGGAAGAAGTCTGCCTTAGACAAATCAGTAAAGTTGTTAAACAAATCAACGACGAGTT 564 TGGAATGGAGAGTTGTGTCACCCTGGGAATGGTTGATAAAGACCAAGCCACTGAATTGAA 516 GAAGTTGGAAACTTGTGTTACTCTCGGGATGATCAACGAAAAGCAGGCTGAAATTTTAAA AAGTGCTGGGTTGACGGCGTACAACCATAACATTGATACTTACAAGGAACACTATCCAAA 684 GGTGATCTCCACAAGAAGCTTTGATGATAGATTGAAAAACATTCAAAAAACGTTCAAAGGATC 636 CGTCGTCACCACCCGTACATACGACGAAGATTAGAAACCATTAAAAACGTCCAAAAAGC 696 TGGTATCAAAGCTTGTACCGGTGGTATTCTCGGATTGGGAGAAACCGCACAAGATCATGT 804 ATCTTTCCTCTACACCTTGGCCACAATGGATCAGCATCCAGAGTCTCTTCCAATCAACAG TTCGTTTTTGTACACTTTGTCCAACATGAGTCCGCACCCAGAATCATTGCCAATCAACAG 864 ACTGGTCCCAATCAAGGGCACGCCAATGTATGAA------GAAGTTAAGAACAA 816 ATTAGTTCCAATCCAGGGTACTCCAATTGTTGAAGTGTTGAAAAATGCACCAAAGGAAAG GCAAGTTGAAGTTGATGAGATTGTCAGAACCATTGCTACTGCAAGATTGGTCATGCCAAC 936 ATCCATCATTAGATTGGCCGCCCGGTCGATACACCATGAAGGAACACGAGCAGTTCTTGTG TGGATTAAAGGCATGCACAGGTGGTATTCTTGGTCTTGGTGAGACCCCAAGAGGACCGTGT 972 GTCTATTATCAGATTGGCTGCAGGAAGATATACAATGAAAGAGGCAGAACAGGTGATGTG CTTCATGGCTGGTTGTAATGCCATCTTCACAGGTAAGAAAATGCTCACACAACAATGTGTAA 1092 CGGCTGGGATGAGGATAAAGCCATGTTGGCTAAATGGGGGTCTGAAACCAATGGAGAGTTT Soybean; biotin synthase; biotin biosynthesis; herbicide; plant development; transgenic plant; ss. Soybean biotin synthase coding sequence #4. Location/Qualifiers ABA01978 standard; cDNA; 1659 BP. 06-FEB-2002 (first entry) CA 1153 CA 1117 max. 507 1032 1152 624 576 744 95/ 912 ABA01978; Glycine RESULT 3 ABA01978 Key 셤 ð ò 요 qq 셤 셤 ò ò ò ઠે 유 ò g ò g 8 셤 ò 음 ઠે 윤 à 셤 8

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              ACATTGATACTTACAAGGAACACTATCCAAAGGTGATCTCCACAAGAAGCTTTGATGATA 712
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SID30.
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19-DEC-2000; 2000US-00740288.
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P-PSDB; ADE76392.
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KINNEY A J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New polypeptides, useful as targets for herbicide discovery, and as probes for genetic and physical mapping of genes of which they are par or creating transgenic plants, comprises biotin synthase polypeptides encoding polynucleotides.
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Pred. No. 1.6e-92;
0; Mismatches 378; Indels
                      /*tag= a
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KINNEY A J.
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OROZCO E M.
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595; Conserv
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                                                                                                      US2001039042-A1
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Best Local S:
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Pred. No. 1.6e-92;
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                                                                                                     Claim 5; SEQ ID NO 29; 47pp; English.
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60.6%;
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                                                                                                                                                                    TGCTCACAACAATGTGTAACGGCTGGGATGAGGATAAAGCCATGTTGGCTAAATGGGGTC 1132
                                                                                                                                                                                                   TGTTAACCACACCACCGTTGGATGGGGTGTCGATTCCGTCGTTTTCAACAGATGGGGAT 1184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Membrane-forming peptide; amphiphilic; monovalent metal cation; suture; internal lining; alow-diffusion drug delivery vehicle; erythropoletin; tissue-type plasminogen activator; hemoglobin; insulin; artificial skin; separation matrix; dialysis membranes; filter; collagen; cell migration; shabimer's disease; scrapie infection; therapy; proteolytic digestion; acidic pH resistant; stomach acid; cell adhesion; cell monolayer; zuotin; tissue culture; differentiated cell; stratified cell layer; de.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence represents the yeast zuctin gene. Fragments of the encoded protein can be used as the amphibhlic peptides used in the macroscopic membrane (MM) of the invention. The NM is formed by self-assembly of the amphibhlic peptides (see AAM30219-W30353) in an aqueous medium containing monovalent metal cations. The NM are stable in serum, are non-yetcoxic, and are useful in biomaterial applications, such as medical products (e.g. sutures), or internal linings. The NM are useful as slow-diffusion drug delivery vehicles for protein-type drugs, including
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                                                                cradaarcercareceraaaccarecerrescratescraecaacaaaaaaaaaaarreace
                                                                                                                     1065 AGGAACAACGTCTTATGTTTCATGGCCGGAGCCAATGCCGTTTTCACAGGAGAACAA
                                  CAAGATTGGTCATGCCAACGTCTATTATCAGATTGGCTGCAGGAAGATATACAATGAAAG
                                                                                                 1013 AGGCAGAACAGGTGATGTGCTTCATGGCTGGTTGTAATGCCATCTTCACAGGTAAGAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Membranes formed by self-assembly of amphiphilic peptide(s) - useful bio:material(s), separation matrices, drug delivery vehicles, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ΰ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lockshin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 5; Col 29-34; 49pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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                                                                                                                                                                                                                                                        TAAGACCCATGGAAAGTTTCGA
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erythropoietin, tissue-type plasminogen activator, synthetic haemoglobin and insulin. They can be used in applications, such as separation matrices (e.g. dialysis membranes). Collagen may be combined with the peptides to produce membranes for use as artificial skin. The MM may be used for making very thin, transparent fabric. Drugs which inhibit the self assembly of the peptides into filaments or filamentous membranes may be useful for treating Alzheimer's disease or scrapie infection. As they as reastant to proteolytic disease into and alkaline and acidic ppH (such as romach acid), drug delivery vehicles made of the MM could be taken orally. The charged residues and conformation of the MM promote cell adhesion and migration. The permeability of the MM also permits diffusion of small molecules, to the underside of cell monolayers, useful for tissue culture of differentiated cells and/or stratified cell layers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATGCCAACGTCTATTATCAGATTGGCTGCAGGAAGATATACAATGAAAGAGGCAGAACAG 1023
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               366 AAGAGTAAAAAGTTGCAATTCGACGAAATTTTGAGAACCATTGCCACAGGGGAATAGTT 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTTGTCTGTTTCATGGCAGGTTGTAACAGTATCTTCACCGGTAAGAAAATGCTGACGACA 545
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                                                                                                                                                                                                                                                                                                                                                                                               2; Length 3083;
                                                                                                                                                                                                                                                                                                                                                 Sequence 3083 BP; 1026 A; 578 C; 627 G; 852 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches 163; Indels
                                                                                                                                                                                                                                                                                                                                                                                               Score 328.2; DB 2
Pred. No. 3.8e-86;
                                                                                                                                                                                                                                                                                                      (Updated on 25-MAR-2003 to correct PF field.)
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72.1%;
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This sequence encodes the human zuctin (ZUO1) protein. Fragments of the protein can be used in the in vitro method of the invention. The method is for culturing cells utilising stable macroscopic membranes formed by the self-assembly of amphiphilic peptides. The peptides are salt-induced to form insolubbe and protease-resistant protein filaments with a beta-sheet secondary structure. The membranes may be may be useful in a wide variety of medical, research, industrial and biomaterial applications such as slow-diffusion drug delivery systems, artificial skin and separation matrices. The membranes may be used to support in vitro cell attachment and growth and for supporting artificial rissue (e.g. for in vivo use as implants). They are particularly useful as experimental models for Alzheimer's disease and scrapie infection and so may be used in disease processes. Additionally, they may be used in this way to study liver cirrhosis, kidney amyloidosis and other protein conformational diseases. The membrane in the membrane/cell mixture conformational diseases. The membrane in the membrane and growth, (ii) self-assembles to form large, macroscopic membranes that are insoluble and stable in a queous solutions, serum and ethanol; (iii) salf-assembles to hard and stable in the method of the disease solutions, serum and ethanol; (iii) salf-assembles to hard and scould and stable in the method of the disease.
                                                         Membrane forming peptide; cell culturing; macroscopic membrane; ambliphilic peptide; alow-diffusion drug delivery system; cell growth; artificial tissue; scrapie infection, Alzheimer's disease; liver cirrhosis; kidney amyloidosis; protein conformational disease; human; zuotin; ZUO1; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    resistant to heat, alkaline/acidic pHs, chemical denaturants and proteolytic digestion; (iv) is non-cytotoxic and non-immunogenic; (v) is visible to the naked eye if dyed but is otherwise transparent; (vi) may
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               form thin, permeable, high density sheets or fibril like structures with simple structures, high tensile strength and a porous structure; (vii) may be metabolised by humans and animals; (viii) is inexpensive to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cell cultures utilizing stable macroscopic membranes formed by the self-assembly of amphiphilic peptides.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         produce; and (ix) can be produced and stored in sterile conditions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3083 BP; 1026 A; 578 C; 627 G; 852 T; 0 U; 0 Other;
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llarity 72.1%; Pred. No. 3.8e-86;
Conservative 0; Mismatches 163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (MASI ) MASSACHUSETTS INST TECHNOLOGY
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                                                                                                                                                                                                                                              Location/Qualifiers
1292. .2593
                                                                                                                                                                                                                                                                                                                    /product= "zuotin"
                     Human zuotin coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       94US-00293284
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nes 445; Conserv
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                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         22-AUG-1994;
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6 GTGAATGATATGGGGCTAGAAACGTGTGTTACTTTAGGTATGGTTGATCAAGATCAAGCA 65

09-NOV-1999 (first entry)

AAZ11218;

RESULT 6 AAZ11218

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Indels

Length 3083;

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                                 732
                                                cacraragraadercarcaccacaadaaccracaacaacacaagararaa
                                                                  792
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                                                                                                                                              366 AAGAGTAAAAAGTTGCAATTCGACGAAATTTTGAGAACCATTGCCACAGCGAGAATAGTT 425
                                                                                                                                                                                                                 605
                                                                                                                    GACGACCATATAGGATTCATCTACACATTATCCAATATGTCTCCTCATCCTGAGTCCCTA 305
                                                                                                                                                                     AAGAACAAGCAAGTTGAAGATTGATGAGAATTGTCAGAACCATTGCTACTGCAAGATTGGTC 963
                                                                                                                                                                                                                                                                                                                                                                                                                                      Macroscopic membrane; biomaterial; medical product; internal lining; artificial skin; slow-diffusion drug delivery; chromatography column; separation marrice; suture; dialysis membrane; viral filter; fabric; pathology; Alzheimer's disease; scrapie infection; yeast; zuotin; ZUO1;
         513 ACTGAATTGAAAAGTGCTGGGTTGACGGCGTACAACCATAACATTGATACTTACAAGGAA
                                CACTATCCAAAGGTGATCTCCACAAGAAGCTTTGATGATAGATTGAAAACATTCAAAAAC
                                                                  GTTCAAGGATCTGGATTAAAGGCATGCACAGGTGGTGTATTCTTGGTCTTGGTGAGACCCAA
                                                                                   GTCCAAGAATCTGGAATAAAAGCCTGTACCGGTGGTATTTTGGGTCTCGGTGAAAGCGAA
                                                                                                    GAGGACCGTGTATCTTTCCTCTACACCTTGGCCACAATGGATCAGCATCCAGAGTCTCTT
                                                                                                                                                                                                                                                                                   CCAATCAACAGACTGGTCCCAATCAAGGGCACGCCAATGTATGAAGAAGTT
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/note= "(AT)7 region"
850. .859
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/note= "T10 region"
950. .958
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/note= "A9 region"
1292. .2593
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/notg= "A9 region"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Saccharomyces cerevisiae.
                                                                                                                                                                                                                                                                                                                                                                                                                      Yeast zuotin (ZUO1) DNA.
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The invention relates to a macroscopic membrane formed by self-assembly of amphiphilic peptides in an aqueous solution containing monovalent metal cations. The peptides have alternating Mydrophobic and hydrophilic amino acids and are complementary and structurally compatible. The membranes are useful as biomaterial for medical products (e.g. sutures, artificial skin, internal linings), as vehicles for slow-diffusion drug delivery (preferably for protein type drugs e.g. erythropoietin, tissue type plasminogen activator, synthetic haemoglobin and insulin), as separation matrices (e.g. dialysis membranes, chromatography columns, filters for the removal of viruses and other microscopic contaminants), for other uses requiring permeable and water-insoluble material (e.g. for culturing cell monolayers including differentiated cells and/or extaitified cell layers), for the preparation of very thin and transparent fabric and as a model system for investigating the properties of biological protein structures and providing insights into the pathology and proteins and proteinaceous structures (e.g. Alzheimer's disease, scrapie infection and in origin of life studies related to cell membranes and cellular comparatementalisation). The present sequence is yeast zuctin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 732
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Macroscopic membrane useful in biomaterial applications e.g. sutures is formed by self-assembly of amphiphilic peptides in an aqueous solution containing monovalent metal cations.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   553 GTCCATGACCTTGGAATGGAGAGTTGTGTCACCCTGGGAATGGTTGATAAAGACCAAGCC
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                                    "Yeast zuotin protein"
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                                                                                                                                                /note= "Homopurine tract'
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2159. .2207
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94US-00346849.
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Best Local Similarity
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P-PSDB; AAE38829
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30-NOV-1994;
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us-09-752-957f-1.rng

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WPI; 2004-356208/33.
P-PSDB; ADO04473.
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22-AUG-1994;
26-MAR-1997;
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                                                                  AAGAGTAAAAAGTTGCAATTCGACGAAATTTTGAGAACCATTGCCACAGGGAGAATAGTT 425
                                                                                                  Argecanagecentraradactrecegerestrararacantenaganacaga 485
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GACGACCATATAGGATTCATCTACACATTATCCAATATGTCTCCTCATCCTGAGTCCCTA 305
                                                                                                                                                                                                                                                                                                                    Macroscopic membrane; cell growth; EAK16; Z-DNA binding protein; zuotin; medical product; suture; artificial skin; internal lining; slow-difficialon drug delivery system; protein-type drug; erythropoietin; haemoglobin; insulin; cell adhesion; cell migration; Alzheimer's disease; scrapie infection; yeast; gene; ds.
                                                                                   ATGCCAACGTCTATTATCAGATTGGCTGCAGGAAGATATACAATGAAAGAGGCAGAACAG
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                                ccaartaaragacracrarcaaaggacrccaarggcrgagacrigccgarcca
                                                  AAGAACAAGCAAGTTGAAGTTGATGAGATTGTCAGAACCATTGCTACTGCAAGATTGGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product= "Yeast Z-DNA binding protein (zuotin)"
2159. .2206
/*tag= i
                 CCAATCAACAGACTGGTCCCAATCAAGGGCACGCCAATGTATGAAGAAGTT
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/note= "7 AT repeats"
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[153. .1162
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The invention relates to a method for in vitro cell culture which involves adding a macroscopic membrane that is formed by self-assembly of amphiphilic peptide in an aqueous solution containing monovalent metal cations to a cell culture medium comprising cells, thus forming a membrane/culture mixture, maintaining the mixture under conditions a sufficient for cell growth. The invention also relates to EAKI6 peptide carried from yeast E-DNA binding protein (zuctin). Zuctin incorporated into the macroscopic membranes are useful in biomaterial applications such as medical products (e.g., sutures), artificial skin or internal linings, slow-diffusion drug delivery systems supports for in vitro cell growth or culture and support for artificial tissue for in vitro use, as slow-diffusion drug delivery vehicle for delivering protein-type drugs conductive biopolymer for culturing cell monolayers, for promoting cell adhesion and migration, useful as experimental models for Alzhaimer's disease and scrapic infection. The present sequence is yeast zuctin DNA. This sequence is used to illustrate the method of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel EAKI6 protein incorporated into macroscopic membranes, useful in biomaterial applications such as medical products, artificial skin or internal linings, slow-diffusion drug delivery systems for in vitro cell
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                                                                                 92US-00973326.
94US-00293284.
97US-00824515.
17-MAR-2003; 2003US-00390472
                                                                                                                                                                                                                                                    (HOLM/) HOLMES T.
(ZHAN/) ZHANG S.
(RICH/) RICH A.
(DDEL/) DIDERAIO C M.
(LOCK/) LOCKSHIN C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cell culture; macroscopic membrane; amphiphilic peptide; biomaterial; slow-diffudion drug delivery system; artificial skin; separation matrix; Alzheimer's disease; scrapie; liver cirrhosis; kidney amyloidosis; protein conformational disease; yeast; DNA binding protein; zuotin; ds;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention describes a method of culturing (M1) cells, in vitro. The cell culture involves adding a macroscopic membrane which is formed by
                                     CCAATTAATAGACTAGTTGCTATCAAAGGGACTCCAATGGCTGAGGAACTTGCCGATCCA
                                                                           <u>AAGAACAAGCAAGTTGAAGTTGATGAGATTGTCAGAACCATTGCTACTGCAAGATTGGTC</u>
                                                                                                            <u> aagagtaaaaagtrigcaartrcgacgaaartrrrgagaaccarrigccacaagagaaragrr</u>
                                                                                                                                                    ATGCCAACGTCTATTATCAGATTGGCTGCAGGAAGATATACAATGAAAGAGGCAGAACAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yeast DNA binding protein zuotin DNA.
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22-AUG-1994;
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monovalent metal cations, where the peptides have alternating hydrophobic and hydrophilic anino acids and are complementary and structurally canno acids and are complementary and structurally compatible, to a cell culture medium comprising cells, thus forming a membrane/culture mixture, and maintaining the mixture under conditions is sufficient for cell growth. (MI) is useful for culturing a macroscopic membrane utilised in biomaterial applications e.g., slow-diffusion drug delivery systems, artificial skin or separation matrices, or as delivery systems, artificial skin or separation matrices, or as cyperimental models for Alzheimer's disease and scrapic infection e.g., liver cirrhosis, kidney amyloidosis, or other protein conformational diseases. (MI) enables in vitro culturing of macroscopic membrane that is stable in aqueous solution, serum and ethanol, highly resistant to heat, alkaline and acidic ph, chemical denaturants and proteolytic diseasin, and is non-cycloxic. This sequence encodes yeast DNA binding protein conformation, and is non-cycloxic. This sequence encodes yeast DNA binding protein conformation and acidic philic peptides capable of forming membrane can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1023
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ATGAAAGGTAGAAAGTCAAACTTGAAGAAAATCAAAAGAGATGATCACTGCTGTCCATGAC
                                                    551 ACCATTGGCAGGAATCAACTTCAACCAGATTCTTGAATATGTCAAGGAAATAAGGGGT
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(KINN/) KINNEY A J.
(MIAO/) MIAO G.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention provides the protein and coding sequences of biotin synthase enzymes from barley, wheat, maize, soybean and the prickly poppy. These sequences can be used to produce transgenic plants which express different levels of the gene, or express it at different times in plant development. They can also be used as a target in the production of herbicides. The present sequence is a maize biotin synthase cDNA obtained from clone cholc.pk009.j14, which was derived from a maize embryo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       wew polypeptides, useful as targets for herbicide discovery, and as probes for genetic and physical mapping of genes of which they are part, or creating transgenic plants, comprises biotin synthase polypeptides and encoding polynucleotides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AACACCTGGACCAAAGAAGAATTAAAGCTATATATGACACACCACTCATGGACTTGATG 261
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                                                                                                                        Maize; biotin synthase; biotin biosynthesis; herbicide; plant development; clone cholc.pk009.j14; transgenic plant;
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Pred. No. 2e-81;
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/product= "biotin synthase"
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                                                                synthase coding sequence #5.
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131. .1264
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Best Local Similarity 59.1%;
Matches 557; Conservative (
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MIAO G.
OROZCO E M.
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                                                                   Maize biotin
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(KINN/) H
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  851 GTAGGGTTGTTGCATACCCTAGCTACCTTGCCTACACACCCCAGAGAGGGGTTCCTATTAAT 910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic; pathway;
                                                                                                    911 GCATTGGTTGCTGTAAAAGGCACACCTCTTGAGG------ACCAGAAGCCTGTAGAG
                                                                                                                                                                                                                                                                                                    GGGCCAACTCCATCTTTGCCGGCGAGAACTTCTCACAACGGCAAACAACGACTTTGAT
                                                   GTTGATGAGATTGTCAGAACCATTGCTACTGCAAGATTGGTCATGCCAACGTCTATTATC
                                                                                                                                                                                                                                                     AGATTGGCTGCAGGAAGATATACAATGAAAGAGGCAGAACAGGTGATGTGCTTCATGGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    promoter; termination sequence; corn; ss
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99US-0134768P.
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19-APR-1999;
21-APR-1999;
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05-MAR-1999
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30-APR-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      441
                                                                                                                                                                                                                                                                                                                      The invention relates to a novel isolated polynucleotide encoding a first polypeptide or a third polypeptide where the first or third polypeptide is a biotin synthase. The methods and compositions of the invention may be useful in plant molecular biology and breading, particularly in the production of altered levels of biotin synthase in plants and seeds. The polypeptides may be used as a target to facilitate the design and/or identification of inhibitors of these enzymes that may be useful as herbicides. Furthermore, the polypuclectides may be used as probes for genetically and physically mapping the genes of which they are a part. The current sequence is that of the corn biotin synthase-related CDNA of
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                                                                                                                                                                     New isolated polynucleotide encoding plant biotin synthase, useful in plant molecular biology and plant breeding purposes, particularly in t production of altered levels of biotin synthase in plants and seeds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 311.8; DB 10; Length
Pred. No. 2e-81;
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59.1%;
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nes 557; Conservative
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(OROZ/) OROZCO E M.
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                                                 Allen SM,
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28-JUL-1999;	02-AUG-1999;	02-AUG-1999; 03-AUG-1999;	04-AUG-1999;	05-AUG-1999;	05-AUG-1999;	06-AUG-1999;	09-AUG-1999;	10-AUG-1999;	11-AUG-1999;	12-AUG-1999;	13-AUG-1999;	16-AUG-1999;	17-AUG-1999; 18-AUG-1999;	20-AUG-1999;	20-AUG-1999; 20-AUG-1999;	23-AUG-1999;	23-AUG-1999;	25-AUG-1999; 26-AUG-1999;	27-AUG-1999;	27-AUG-1999;	27-AUG-1999;	31-AUG-1999;	01-SEP-1999;	07-SEP-1999;	13-SEP-1999;	15-SEP-1999;	16-SEP-1999;	22-SEP-1999;	23-SEP-1999;	28-SEP-1999;	29-SEP-1999;	05-OCT-1999;	06-OCT-1999;	07-OCT-1999; 08-OCT-1999;	12-OCT-1999;	13-OCT-1999;	13-0CT-1999;	14-OCT-1999;	14-0CT-1999;	14-0CT-1999;	18-OCT-1999; 18-OCT-1999;	21-OCT-1999;	21-OCT-1999;	21-0CT-1999;	21-OCT-1999;	21-OCT-1999; 22-OCT-1999;	22-OCT-1999;	22-OCT-1999; 25-OCT-1999;	25-OCT-1999;	25-0CT-1999; 26-0CT-1999;
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New polypeptides, useful as targets for herbicide discovery, and as probes for genetic and physical mapping of genes of which they are, part, or creating transgenic plants, comprises biotin synthase polypeptides and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention provides the protein and coding sequences of biotin synthase enzymes from barley, wheat, maize, soybean and the prickly poppy. These sequences can be used to produce transgenic plants which express different levels of the gene, or express it at different times in plant development. They can also be used as a target in the production of herbicides. The present sequence is a barley biotin synthase CDNA obtained from clone bsh1.pk0005.d10, which was derived from a barley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    273 TICCACGGGGCTCAAGTCCATAGGAATGTCCATAAATTTAGAGAAGTGCAAATATGCACA 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            202 AACACCTGGACCAAAGAAGAAATTAAAGCTATATATGACACACCACTCATGGACTTGATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        262 CACTATGCTCAGGTGCAACACAGAAGGTTCCAACAACACCTTCAGAGGTTCAATTGTGCACT
                                                                                                                                                                                               Barley, biotin synthase, biotin biosynthesis, herbicide, seedli
plant development, clone bshl.pk0005.d10, transgenic plant, ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1396 BP; 387 A; 351 C; 356 G; 302 T; 0 U; 0 Other;
1072 GCGGACCAGGCGATGTTCAAGATCCTTGGCCTGATCCCCAAGG 1114
                                                                                                                                                                                                                                                                                                                                                     start codon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 310.2; DB 6;
Pred. No. 5.6e-81;
0; Mismatches 378;
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/note= "the sequence has no
                                                                                                                                                                                                                                                                                                                       synthase"
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                                                                                                                                                                  Barley biotin synthase coding sequence #2
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/*tag= a
/product= "biotin
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                                                                         ABA01972 standard; cDNA; 1396
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KINNEY A J.
MIAO G.
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P-PSDB; AAM51979.
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es 556; Conserv
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4; Mismatches 377
                                                                                                       26.1%; Score 310.2; 58.6%; Pred. No. 5.4
           990S-0161361P.
990S-0161920P.
990S-0161992P.
990S-0161993P.
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ALLEN S M. KINNEY A J. MIAO G.

OROZCO B M.

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New isolated polynuclectide encoding plant biotin synthase, useful in plant molecular biology and plant breeding purposes, particularly in production of altered levels of biotin synthase in plants and seeds.
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                                                                                                                                                 21-DEC-1999; 99US-0172929P.
19-DEC-2000; 2000US-00740288.
                                                                                   07-MAY-2003; 2003US-00431544
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P-PSDB; ADE76380.
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The invention relates to a novel isolated polynucleotide encoding a first polypeptide or a third polypeptide where the first or third polypeptide is a biotin synthase. The methods and compositions of the invention may be useful in plant molecular biology and breeding, particularly in the production of altered levels of biotin synthase in plants and seeds. The polypeptides may be used as a target to facilitate the design and/or identification of inhibitors of these enzymes that may be useful as herbicides. Furthermore, the polymucleotides may be used as probes for genetically and physically mapping the genes of which they are a part.
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                                                                                                                                                                                                                                                                                                                                                                                                       202 AACACCTGGACCAAAGAAGAAATTAAAGCTATATATGACACACCACTCATGGACTTGATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            262 CACTATGCTCAGGTGCAACACAGAAGGTTCCAACAACCTTCAGAGGTTCAATTGTGCACT
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                                                                                                                                                                                                                                                                                                                     DB 10; Length 1396;
                                                                                                                                                                                                                                                                       Sequence 1396 BP; 387 A; 351 C; 356 G; 302 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                Score 310.2; DB 10;
Pred. No. 5.6e-81;
0; Mismatches 378;
                                                                                                                                                                                                                                                                                                                26.1%;
59.0%;
                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 59.0
Matches 556; Conservative
                                                                                                                                                                                                                                                                                                                                         Local Similarity
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plant; breeding; seed; herbicide; ss; gene; barley;

E - SEQ

biotin synthase cDNA

SID18

Barley

biotin synthase;

SID18.

Hordeum vulgare. US2003192073-A1

(first entry)

29-JAN-2004

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standard; cDNA; 1396

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The present invention provides the protein and coding sequences of biotin synthase enzymes from barley, wheat, maize, soybean and the prickly poppy. These sequences can be used to produce transgenic plants which express different levels of the gene, or express it at different times in plant development. They can also be used as a target in the production of herbicides. The present sequence is a maize biotin synthase cDNA obtained from clone cca.pk0012.g11:fis
probes for genetic and physical mapping of genes of which they are part, or creating transgenic plants, comprises biotin synthase polypeptides and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   982 AGATTGGCTGCAGGAAGATATACAATGAAAGAGGCAGAACAGGTGATGTGCTTCATGGCT 1041
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CACTATGCTCAGGTGCAACACAGAAGGTTCCAACAACCTTCAGAGGTTCAATTGTGCACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              595 ATGGGCATGGAGGTCTGTTGCACACTAGGCATGATAGAGAAACAACAAGCTGAAGAACTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      655 AAGAAGGCTGGACTTACAGCATATAATCATAACCTAGATACATCAAGAGAGTATTATCCC
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                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                  26.1%; Score 310.2; DB 6; ilarity 59.0%; Pred. No. 5.7e-81; Conservative 0; Mismatches 378;
                                                                                        Claim 5; Page 29-30; 46pp; English.
                          or creating transgenic plancoding polynucleotides.
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nes 556; Conserv
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                                                                                                                                                                                                       861
                                                                                                                                                                                                                                                                                                  921
                                                                                                                                                                                                                                                                                                                                          GCATTGATTGCTGTCAAAGGCACGCCTCTTCAGG-----ATCAGAAGCCTGTAGAG 923
                                                                                                                                                                                                                                                                                                                                                                                          GTTGATGAGATTGTCAGAACCATTGCTACTGCAAGATTGGTCATGCCAACGTCTATTATC 981
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                                                                                                                                                                                                     GTATCTTTCCTCTACACCTTGGCCACAATGGATCAGCATCCAGAGTCTCCTTCCAATCAAC
                                                                                                                                                                                                                                                                                                  <u>AAGGTGATCTCCACAAGAAGCTTTGATGATAGATTGAAAACGTTCAAAAACGTTCAAGGA</u>
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                                                                                                               TCTGGATTAAAGGCATGCACAGGTGGTATTCTTGGTCTTGGTGAGACCCAAGAGGACCGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         plant;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 herbicide;
transgenic
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/*tag= a
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OROZ-
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8236.851 Million cell updates/sec US-09-752-957F-1 1188 1 atgtcgtttatattgactgc.....aggttgcattcggtgcttga 1188 Perfect score: Run on:

IDENTITY NUC Gapext 1.0 Scoring table: Sequence:

1202784 seqs, 818138359 residues Searched:

2405568 Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 200000000

1: /cgn2 6/ptodata/1/ina/5A COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/PcTUS_COMB.seq:* Issued Patents NA:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		*			SUMMARIES	
Result No.	Score	Query	Length 1	DB	ΩI	Description
1	414.4	34.9	1263	4	US-09-248-796A-4445	Sequence 4445, Ap
	328.2	27.6	3083	-	US-08-346-849-1	'n
m	328.2	27.6	3083	~	US-08-293-284A-1	'n
4	328.2	27.6	3083	4	US-08-898-300-1	۲,
S	328.2	27.6	3083	4	US-08-824-513-1	٦,
9	304	25.6	1351	~	US-08-401-068-13	13,
7	304	25.6	1351	7	US-08-846-338-13	13,
æ	236	19.9	1017	4	US-09-328-352-2698	2698
o		19.4	954	4	US-09-902-540-7391	7391,
c 10	230.4	19.4	4183	4	US-09-902-540-709	709, #
11	211.6	17.8	1830121	4	US-09-557-884-1	1,
12	211.6	17.8	1830121	4	US-09-643-990A-1	-
c 13	208.2	17.5	1230025	4	US-09-198-452A-1	,
c 14	208.2	17.5	1230230	4	US-09-438-185A-1	ų
15	205.2	17.3	1420	ო	US-09-180-109A-23	23
16	203.6	17.1	1336	٣	US-09-180-109A-28	28,
c 17	200	16.8	640681	4	US-09-790-988-1	٦,
18	198.8	16.7	1053	4	US-09-543-681A-1175	Ξ
19	195.2	16.4	1182	4	US-09-252-991A-3220	Sequence 3220, Ap
o 20	195.2	16.4	3150	4	US-09-252-991A-3348	334
21	193.8	16.3	1041	~	US-08-401-068-7	7,
22	193.8	16.3	1041	7	US-08-846-338-7	7,
23	192.4	16.2	5872	۳	US-08-411-768B-1	ť
24	192.4	16.2	5872	ო	US-08-411-768B-6	6, 7
25	191	16.1	1358	ش	US-09-180-109A-25	22,
26	186.4	15.7	3501	4	-60-	70,
c 27	184.2	15.5	34001	4	US-09-596-002-18	18,

Sequence 5954, Ap Sequence 1834, Ap Sequence 338, App	Sequence 338, App Sequence 7, Appli Sequence 7, Appli		Sequence 634, App Sequence 539, App Sequence 3541, Ap	Sequence 3895, Ap Sequence 2561, Ap Sequence 3934, Ap	Sequence 14, Appl Sequence 1, Appli
US-09-489-039A-5954 US-09-540-236-1834 US-08-956-171E-338	US-08-781-986A-338 · US-08-935-263-7 US-09-594-1185-7	US-08-676-818-1 US-09-407-549-1 US-09-633-927-1	US-09-134-001C-634 US-09-710-279-539 US-09-710-279-3541	US-09-710-279-3895 US-09-710-279-2561 US-09-710-279-3934	US-08-232-463-14 US-08-916-421B-1
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ALIGNMENTS

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Sequence 4445, Application US/09248796A

Sequence 4465, Application US/09248796A

Patent No. 6747137

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION:
FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION:
FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION WHERE: US/09/248,796A
CURRENT APPLICATION WHERE: US 60/074,725
PRIOR PELLING DATE: 1998-02-13
PRIOR FILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 4445
LENGTH: 1263
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Pred. No. 3.4e-122;
0; Mismatches 301;
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Best Local Similarity 66.8%;
Matches 643; Conservative
                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Candida albicans
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Pred. No. 2.9e-94;
0; Mismatches 163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: 1292..2590
OTHER INFORMATION: /product= "zuotin"
                                                                                                          NAME: Brook, David E.
REGISTRATION NUMBER: 22,592
REFERNICE/DOCKET NUMBER: MIT-6008
TELEPHONE: (617) 861-6240
TELEPHONE: (617) 861-6240
INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 3083 base pairs
               PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/973,326.
FILING DATE: 28 DECEMBER 1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1144 GAGAGTTTCAAATACAA 1160
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MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27.6%;
                                                                                                                                                                                                                                                                                                       LENGTH: 3083 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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Best Local Similarity 72.1
Matches 445; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        954 ATTAGTTCCAATCCAGGGTACTCCAATTGTTGAAGTGTTGAAAAATGCCCCAAAGGAAAG 1013
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                                                                                                                                                                                                                                                                                                                                                                                                                    TTCGTTTTTGTACACTTTGTCCAACATGAGTCCGCACCCAGAATCATTGCCAATCAACAG 953
                                          654 GAAGTTGGAAACTTGTGTTACTCTCGGGATGATCAACGAAAAGCAGGCTGAAATTTTAAA 713
                                                                                                                                      714 Acagaariegririgacrieccracaacacarirgacacrircaagagaacarrarccaaa 773
                                                                                                                                                                                        GGTGATCTCCACAAGAAGCTTTGATGATAGATTGAAAACATTCAAAAACGTTCAAGGATC 743
                                                                                                                                                                                                                                      cercercaccacceracaraceaceaaagarragaaaccarraaaaacerccaaaaage 833
                                                                                                                                                                                                                                                                                                                                                                                   804 ATCTTTCCTCTACACCTTGGCCACAATGGATCAGCATCCAGAGTCTTCCAATCAACAG 863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACTGGTCCCAATCAAGGGCACGCCAATGTATGAAGAAGT-------TAAGAACAA 911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   912 GCAAGTTGAAGTTGATGAGATTGTCAGAACCATTGCTACTGCAAGATTGGTCATGCCAAC 971
564 TGGAATGGAGAGTTGTGTCACCCTGGGAATGGTTGATAAAGACCAAGCCACTGAATTGAA
                                                                                                                                                                                                                                                                                                               TGGATTAAAGGCATGCACAGGTGGTATTCTTGGTCTTGGTGAGACCCAAGAGGACCGTGT
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PEPTIDES AND USES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Zhang, Shuguang
APPLICANT: Lockshin, Curtis
APPLICANT: Rich, Alexander
APPLICANT: Rich, Alexander
APPLICANT: Rich, STABLE MACROSCOPIC MEMBRANES FORM
TITLE OF INVENTION: SELF-ASSEMBLY OF AMPHIPHILIC PEPT
TITLE OF INVENTION: BELF-ASSEMBLY OF AMPHIPHILIC PEPT
TITLE OF INVENTION: BELF-ASSEMBLY OF AMPHIPHILIC PEPT
TITLE OF INVENTION: BEREFOR NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: HAMILTON, BROOK
STREET: TWO MillION BROOK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/346,849
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/08346849
Patent No. 5670483
GENERAL INFORMATION:
APPLICANT: Zhang, Shuguang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lexington
Massachusetts
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ZIP: 02173-4799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CA 1255
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US-08-346-849-1
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STATE:
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1083

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605

852

903

792

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1084 ATGTGTAACGGCTGGGATGAGGATAAAGCCATGTTGGCTAAATGGGGTCTGAAACCAATG 1143
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                                                                                                                                                                                                                                                                                 964 ATGCCAACGTCTATTATCAGATTGGCTGCAGGAAGATATACAATGAAAGAGGCCAGAACAG 1023
                                         246 GACGACCATATAGGATTCATCTACACATTATCCAATATGTCTCCTCATCCTGAGTCCCTA 305
                                                                                                                                       366 AAGAGTAAAAAGTTGCAATTCGACGAAATTTTGAGAACCATTGCCACAGGGAATAGTT 425
                                                                                                                                                                                                                                                                                                                              546 ATATATAACGGTTGGGACGAAGACAAGGCAATGTTGGCTAAATGGGGATTGCAACCTATG 605
                                                                                                                                                                                      904 AAGAACAAGTTGAAGTTGATGAGATTGTCAGAACCATTGCTACTGCAAGATTGGTC
                                                                                                                                                                                                                                                                                                                                                                                                                           486 TTTGTCTGTTTCATGGCAGGTTGTAACAGTATCTTCACCGGTAAGAAAATGCTGACGACA
793 GAGGACCGIGTATCTTTCCTCTACACCTTGGCCACAATGGATCAGCATCCAGAGTCTCTT
                                                                                        853 CCAATCAACAGACTGGTCCCAATCAAGGGCACGCCAATGTATGAAGAAGTT-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STABLE MACROSCOPIC MEMBRANES FORMED BY
SELF-ASSEMBLY OF AMPHIPHILIC PRPTIDES AND USES
THEREFOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER FEADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Elappy disk
COMPUTER: Elappy disk
COMPUTER: Elap PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/898,300
FILING DATE: 22 JULY 1997
CLASSIFICATION NUMBER: 08/346,849
FILING DATE: 30 NOVENBER 1994
PRIOR APPLICATION NUMBER: 07/973,326
FILING DATE: 28 DECEMBER 1992
ATPONEY/AGENT INFORMATION:
ANDE: LABELICATION NUMBER: 07/973,326
FILING DATE: 28 DECEMBER 1992
ATPONEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 22,592
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: MIT-6008FB
TELECOMUNICATION INFORMATION:
TELEPANE: (781) 861-6240
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 1, Application US/08898300
; Patent No. 6548630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1144 GAGAGTTTCAAATACAA 1160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Zhang, Shuguang
APPLICANT: Lockshin, Curtis
APPLICANT: Rich, Alexander
APPLICANT: Holmes, Todd
TITLE OF INVENTION: STABLE MAC
TITLE OF INVENTION: THEREFOR
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: HAMILTON, BROOK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GAGGCATTTAAGTACGA 622
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: Two Mili
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: U.S.A. ZIP: 02173-4799
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                613 ACTGAATTGAAAAGTGCTGGGTTGACGGCGTACAACCATAACATTGATACTTACAAGGAA 672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAGCAATTGAAAGATGCAGGTTTGACTGCATACAACCATAACATCGACACTTCCAGAGAA 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GICCAAGAAICIGGAAIAAAAGCCIGIACCGGIGGIAITITIGGGICICGGIGAAAGCGAA 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CACTATCCAAAGGTGATCTCCACAAGAAGCTTTGATGATAGATTGAAAACATTCAAAAAC 732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        733 GTTCAAGGATCTGGATTAAAGGCATGCACAGGTGGTATTCTTGGTCTTGGTGAGACCCAA 792
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                                                                                                          APPLICANT: Holmes, Todd
APPLICANT: Alexander
APPLICANT: Zhang, Shuguang
APPLICANT: Rich, Alexander
APPLICANT: DiPersio, C. Michael
APPLICANT: DiPersio, C. Michael
APPLICANT: Lockshin, Curtis
TITLE OF INVENTION: STABLE MACROSCOPIC MEMBRANES FORWED BY
TITLE OF INVENTION: THEREFOR
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2; Length 3083;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27.6%; Score 328.2; DB 2; Length 72.1%; Pred. No. 2.9e-94; Live 0; Mismatches 163; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/293,284A
FILING DATE: 22-AUG-1994
CLASSITCATION: 435
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/973,326
FILING DATE: 22-B-DEC-1992
ATTORNEY/AGENT INFORMATION:

NAME: BLOCK, DAVIG E.

REFERENCE/DOCKET NUMBER: MIT-6008A
TELEPHONE: (617) 861-6240
TELEPHONE: (617) 861-6540
INFORMATION FOR SEQ ID NO: 1:
SEQUINCE CHARACTERISTICS:

SEQUINCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
STREET: Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: CDS
LOCATION: 1292..2590
OTHER INFORMATION: /product= "zuotin"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 02173.4799
COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                            Sequence 1, Application US/08293284A Patent No. 5955343 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3083 base pairs
                                                                                                                                                                                                                                                                                                                                                                             STREET: Two Militia Dr
CITY: Lexington
STATE: Massachusetts
COUNTR: U.S.A.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CENGTH:
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613 ACTGAATTGAAAAGTGCTGGGTTGACGGCGTACAACCATAACATTGATACTTACAAGGAA 672
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CACTATCCAAAGGTGATCTCCACAAGAAGCTTTGATGATAGATTGAAAACATTCAAAAAC 732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       126 CACTATAGTAAGGTCATCACCACGAGAACCTACGACAGGGTTACAGACCATCAAGAAT 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GITCAAGGATCTGGATTAAAGGCATGCACAGGTGGTATTCTTGGTCTTGGTGAGACCCAA 792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      186 Grccaagaarcregaaraaagccreraccegregrarrregercregreaaagcgaa 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            793 GAGGACCGTGTATCTTTCCTCTACACCTTGGCCACAATGGATCAGCATCCAGAGTCTT 852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GACGACCATATAGGATTCATCTACACATTATCCAATATGTCTCCTCATCCTGAGTCCCTA 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CCAATCAACAGACTGGTCCCAATCAAGGGCACGCCAATGTATGAAGAAGTT----- 903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             904 AAGAACAAGCAAGTTGAAGTTGATGAGATTGTCAGAACCATTGCTACTGCAAGATTGGTC 963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTGAATGATATGGGGCTAGAAACGTGTGTTACTTTAGGTATGGTTGATCAAGATCAAGCA 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   553 GTCCATGACCTTGGAATGGAGAGTTGTGTCACCCTGGGAATGGTTGATAAAGACCAAGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                     BROOK, SMITH & REYNOLDS, P.C.
                                                                                                                                                                                                              CAMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Elb PC compatible
COMPUTER: Elb PC compatible
COMPUTER: TEM PC compatible
COMPUTER: TEM PC COMPATIBLE
COMPUTER: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/824,513
FILING DATE: March 26, 1997
CLASSIFICATION NUMBER: 08/293,284
FILING DATE: August 22, 1998
FILING DATE: August 23, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27.6%; Score 328.2; DB 4; 72.1%; Pred. No. 2.9e-94; tive 0; Mismatches 163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; LOCATION: 1292..2590
; OTHER INFORMATION: /product= "zuotin"
US-08-824-513-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: MIT-6008A2 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (781) 861-6240
TELEPAX: (781) 861-9540
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3083 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 27.6
Best Local Similarity 72.1
Matches 445; Conservative
                             CORRESPONDENCE ADDRESS:
ADDRESSEE: HAMILION,
STREET: Two Militia D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                      Massachusetts
                                                                                         CITY: L. BEBELL
STATE: MASSELL
COUNTRY: U.S.A.
T.D: 02173-4799
  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              246 GACGACCATATAGGATTCATCTACACATTATCCAATATGTCTCCTCATCTGAGTCCCTA 305
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                                                                                                                                                                                                                                                                                                                                                                                                                                      553 GTCCATGACCTTGGAATGGAGATTGTGTCACCCTGGGAATGGTTGATAAAGACCAAGCC

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Zhang, Shuguang
Rich, Alexander.
DiPersio, C. Michael
Lockshin, Curtis
WRENTION: STABLE MACROSCOPIC MEMBRANES FORMED BY
VENTION: STABLE MACROSCOPIC MEMBRANES FORMED BY
VENTION: THEREFOR
                                                                                                                                                                                                                                                                                                                                                                             6
                                                                                                                                                                                                                                                                                                                       DB 4; Length 3083;
                                                                                                                                                                                                                                                                                                                    27.6%; Score 328.2; DB 4; Length 72.1%; Pred. No. 2.9e-94; ive 0; Mismatches 163; Indels
                                                                                                                                                                                                  ; LOCATION: 1292..2590
; OTHER INFORMATION: /product= "zuotin"
US-08-898-300-1
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Patent No. 6800481
GENERAL INFORMATION:
APPLICANT: Holmes, Todd
APPLICANT: Zhang, Shuguang
APPLICANT: Rich, Alexander
APPLICANT: Lockshin, Curtis
TITLE OF INVENTION: STABLE MACROSC
TITLE OF INVENTION: THEREFOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1144 GAGAGTTTCAAATACAA 1160
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                                                                                      TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
LENGIH: 3083 base pairs
                                                                                                                                                                                                                                                                                                                                                                                Matches 445; Conservative
                             TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
                                                                                                                                               FEATURE:
NAME/KEY:
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                                                                                    254 Trocardeaecroagerroaradacareiroaraactroagedagiadaacaarerade 313
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                             CACTATGCTCAGGTGCAACACAGAAGGTTCCAACAACAACTTCAGAGGTTCAATTGTGCACT
                                                                                                                                                                                                                                                                            CGTTACAACACTGGTGTCAAGGCTGAAAGAATCATCCAAGTTGATGAGGTGATTGAAGCT
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STREET: 520 White Plains Road, P.O. Box 2005
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Patent No. 5869719
GENERAL INFORMATION:
APPLICANT: Patton, David
TITLE OF INVENTION: Transgenic Pl
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                         ATGTGTAACGGCTGGGATGAGGATAAAGCCATGTTGGCTAAATGGGGGTCTGAAACCAATG 1143
                                                                                                                                                                                     1024 GTGATGTGCTTCATGGCTGGTTGTAATGCCATCTTCACAGGTAAGAAAATGCTCACAACA 1083
                                                                                                 486 Tritgicrigitratgacaagitrataacagiarcircaccagiaagaaargcigacaaaas
                                                                                                                                                                                                                                                                                                                                                   36 AAGAGTAAAAAGTTGCAATTCGACGAAATTTTGAGAACCATTGCCACAGCGAGAATAGTT 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     194 AACGATTGGAGTAGAGATGAAATCAAGTCTGTTTATGATTCTCCTCTTCTTGACCTCCTC 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AACACCTGGACCAAAGAAAATTAAAGCTATATATGACACACCACTCATGGACTTGATG
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; OTHER INFORMATION: /product= "Arabidopsis BioB enzyme"
US-08-401-068-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches 380; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Version #1.30B
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Pred. No. 1e-86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 13, Application US/08401068
Patent No. 5859335
GENERAL INFORMATION:
APPLICANT: Patton, David
TITLE OF INVENTION: Enhanced Biotin Bi
CORRESPONDENCE ADDRESS:
ADDRESSEE: CIBA-GEIGY Corporation
STREET: 7 Skyline Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 415
PRIOR APPLICATION DATA:
APPLICATION UNDBER: US 08/351,970
FILING DATE: 08-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Elmer, James Scott
REGISTRATION UNDBER: 36,129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Parentln Release #1.0, CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/401,068 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                    GAGAGTTTCAAATACAA 1160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAGGCATTTAAGTACGA 622
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58.6%;
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1351 base pairs
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Best Local Similarity
Matches 551; Conserv
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HYPOTHETICAL:
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US-08-401-068-13
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Sequence 2698, Application US/09328352

Sequence 2698, Application US/09328352

Patent No. 6562958

GREERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT RILING DATE: 1999-06-04

NUMBER OF SEQ ID NOS: 8252

SEQ ID NO 2698
LENGTH: 1017
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742 TCTGGATTAAAGGCATGCACAGGTGGTATTCTTGGTCTTGGTGAGACCCAAGAGGACCGT 801
                                                                                                                                                                                                                               854 GCTCTACTTGCAGTGAAAGGCACTCCTCTTGAAG------ACCAGAAGCCAGTTGAG 904
                                                                                                                                                                                                                                                                             GTIGATGAGATIGICAGAACCATIGCTACTGCAAGATIGGTCATGCCAACGTCTATTATC 981
                                                                                                                                                                                                                                                                                                                        905 arargegagiaricadegargaricanaccicacicariteraricanangcanggang 964
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                                                                                       GTATCTTTCCTCTACACCTTGGCCACAATGGATCAGCATCCAGAGTCTTCCAATCAAC
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US-09-328-352-2698
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US-09-328-352-2698
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CACTATGCTCAGGTGCAACACAGAAGGTTCCAACAACCTTCAGAGGTTCAATTGTGCACT 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCTAAGAAGGCAAAAGAAGCTGGGAGCACACACTTTTTGCATGGGTGCTGCTTGGCGAGAT 493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATGAAAGGTAGAAAGTCAAACTTGAAGAAAATCAAAGAGATGATGACTGCTGTCCATGAC 561
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAAAGTGCTGGGTTGACGGCGTACAACCATAACATTGATACTTACAAGGAACACTATCCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: 59..1192
; OTHER INFORMATION: /product= "Arabidopsis biotin synthase enzyme"
US-08-846-338-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25.6%; Score 304; DB 2; Length 1351; 58.6%; Pred. No. 1e-86; ive 0; Mismatches 380; Indels
                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/646,338
                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 13:15 base pairs
TYPE: nucleic acid
STRANDENNESS: single
                                                                                                                                                                                                                                                                                                                                                        38.241
                                                                                                                                                                                                                                                                               CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 58.6
Matches 551, Conservative
                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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         Tarrytown
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                                                  USA
                                                                                                                                                                                                                                                            FILING DATE:
                                                                      10591
                        STATE: N
COUNTRY:
ZIP: 105
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                                                                                                                                                                                             CAAGACGGGCGTCAAGGCGGAGAAGCTGATGGCCGTGCCGGACGTGCTGGATGCCGCGTC 248
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; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wingland, Roger C.
; TILLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof; FILE REFERENCE: 38-10(15849)E
; FILE CAPICANT: WINGBER: US/09/902,540
267 TGCTCAGGTGCAACACAGAAGGTTCCAACAACCTTCAGAGGTTCAATTGTGCACTCTTAT
                                                                                                                                                        CAACACTGGTGTCAAGGCTGAAAGAATCATCCAAGTTGATGAGGTGATTGAAGCTGCAAA
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                                                                           GAATATCAAAACTGGTGGTTGTACCGAGGACTGTAAGTACTGTGCCCAATCACAGCGTTA
                                                                                                               <u>erccarcaacacecececececaacacerecrectacecececacecececere</u>
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                                    <u> GGCCCAGACGGTCCACCGGGCCGTGTTCGTGGACAACAAGGTCCAGCTCTGTTCGCTGCT</u>
                                                                                                                                                                                                                                   TGCTGGGTTGACGGCGTACAACCATAACATTGATACTTACAAGGAACACTATCCAAAGGT
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US-09-902-540-709/c
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                                                                           GCCACTGAATTGAAAAGTGCTGGGTTGACGGCGTACAACCATAACATTGATACTTACAAG 669
                                                                                                                                                      GCAGAACGCCTAAAAGATGCCGGTTTAGACTATTACAACCATAACCTTGATACTTCTCGC 501
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                                                                                                                                                                                                                                                                                                                                                                                                                                     CTTCCAATCAACAGACTGGTCCCAATCAAGGGCACGCCAATGTATGAAGAAGTTAAGAAC 909
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GCTTGGCG-----CAACCCTCATGAGCGCGATATGCCTTATGTTTTAGAAATGGTACGT 381
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                                      GCTGTCCATGACCTTGGAATGGAGGTTGTGTCACCCTGGGAATGGTTGATAAAGACCAA
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Pred. No. 3.6e-63;
0; Mismatches 416;
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Patent No. 6813447

GENERAL INFORMATION:

APPLICANT: Goldman, Barry S.

APPLICANT: Slater, Steven C.

APPLICANT: Wiegand, Roger C.

TITLE OF INVENTION: Myxococcus xanthus Genome Seq:

FILE REPERENCE: 38-10(15849)B

CURRENT APPLICATION UNDBER: US/09/902,540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 7391
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ORGANISM: Myxococcus xanthus
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Best Local Similarity 54.5
Matches 512; Conservative
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US-09-902-540-7391
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CITY: Rockville
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COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                            Length 4183;
                                                                                                                                                                                                                                                                                                                                                        Score 230.4; DB 4; Length Pred. No. 9.1e-63; 0; Mismatches 416; Indels
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 709
                                                                                                                                                                                                                                                                                                                                                        19.4%;
54.5%;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                       Genome,
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1107 TARAGCCATGTTGGCTRAATGGGGTCTGAAACCAATGGAG 1146
                                            1239 chrodecerderidaagaadageeddaaneegeedeeridaag 1200
                                                                                                                                                                                                                                                                                                  Rd
                                                                                                                                                                      Sequence 1, Application US/09557884
Patent No. 6506581
GENERAL INFORMATION:
APPLICANT: Fleischmann et al.
APPLICANT: Fleischmann et al.
TITLE OF INVENTION: The Nucleotide sequence of
TITLE OF INVENTION: The Themophilus influenzae
Thereof, and Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17.8%; Score 211.6; DB 4;
llarity 54.3%; Pred. No. 4.7e-55;
Conservative 0; Mismatches 404;
                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESSE:
ADDRESSE: Human Genome Sciences,
STREET: 9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/09/557,884
FLING DATE: 25-Apr-2000
CLASSIFICATION: «UNKNOWN»
NPPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: 3 1/2 inch diskette
COMPUTER: Dell Pentium
OPERATING SYSTEM: MS DOS v6.22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 08/476,102
FILING DATE: JUN-5-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
TOPOLOGY: linear
;
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-557-884-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Michelle S. Marks
REGISTRATION NUMBER: 41,971
REFERENCE/DOCKET NUMBER: PB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: 301-309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 301-309-8439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 1830121 base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: ASCII TEXT CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1085962 GTACCTTTGGTTTATTGCAAGACGGTATGGCGGAAGATTTAAAAGAAGCTGGATTAGATT 1086021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1085608 AAGTIGAGGGGTTATTTGAAAGGCCATTTTTGGAATTTAGTTTACGGAGCAAGGTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1085668 ArcGrAAGCATTTTAATCCTCGCGCATTCAGTTATCCACGTTAATGTCTATCAAAACGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     581 TCACCCTGGGAATGGTTGATAAAGACCAAGCCACTGAATTGAAAAGTGCTGGGTTGACGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       281 ACAGAAGGTTCCAACAACCTTCAGAGGTTCAATTGTGCACTCTTATGAATATCAAAACTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTGGTTGTACCGAGGACTGTAAGTACTGTGCCCAATCACAGCGTTACAACACTGGTGTCA
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54.3%; Pred. No. 4.7e-55;
tive 0; Mismatches 404;
                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/487,429
FILING DATE: 1995-06-07
APPLICATION NUMBER: 08/426,787
FILING DATE: 1995-04-21
ATTORNEY/AGENT INFORMATION:
NAME: Kenley K. Hoover
REGISTRATION NUMBER: 40,302
REFERENCE/DOCKET NUMBER: PB186FDC1
                   APPLICATION NUMBER: US/09/643,990A
FILING DATE: 23-Aug-2000
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 1830121 base pairs
                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: 301-610-5790
                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 310-309-8439
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: double
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
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Best Local Similarity 54.3
Matches 500; Conservative
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  1085848 GTGGTGCAGGGCGTTTCTGTATGGGGGCTGCTTGGCGAGGCCCTAAGCCAA-----AAG 1085901
                                                                                                     ATATTGAGAAAGTCACAGAAATTATTAAAGCCGTGAAATCACTTGGTTTAGAAACTTGCG 1085961
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Thereof, and Uses Thereof
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                                                        ACTIGAAGAAAATCAAAGAGAIGAICACIGCIGICCAIGACCIIGGAAATGGAGAGTIGIG
                                                                                                                                                                 TCACCCTGGGAATGGTTGATAAAGACCAAGCCACTGAATTGAAAAGTGCTGGGTTGACGG
                                                                                                                                                                                                              1085962 GTACCTTTGGTTTATTGCAAGACGGTATGGCGGAAGATTTAAAAGAAGCTGGATTAGATT
                                                                                                                                                                                                                                                                         CGTACAACCATAACATTGATACTTACAAGGAACACTATCCAAAAGGTGATCTCCACAAGAA
                                                                                                                                                                                                                                                                                                                                                                                  GCTTTGATGATAGATTGAAAACATTCAAAAACGTTCAAGGATCTGGATTAAAGGCATGCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATACAATGAAAGAGGCAGAACAGGTGATGTGCTTCATGGCTGGTTGTAATGCCATCTTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAGGTAAGAAATGCTCACAACAATGTGTAACGGCTGGGATGAGGATAAAGCCATGTTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hamilton O. Smith
J. Craig Venter
TITLE OF INVENTION: The Nucleotide sequence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: 3 1/2 inch diskette COMPUTER: Dell Pentium OPERATING SYSTEM: MS DOS v6.22 SOFTWARE: ASCII Text
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1086492 CAAAATTAGATTTAGAGCCA 1086511
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Mark D. Adams
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTAAATGGGGTCTGAAACCA 1140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/09643990A Patent No. 6528289 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1086261 Gracecerrascesarsess
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ZIP: 20850
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Owen White
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US-09-643-990A-1
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NAME/KEY: misc feature
LOCATION: (330001). (345000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (345001)..(360000)
OTHER INFORMATION: n=a or c or g or t
LOCATION: (360001)..(35000)
OTHER INFORMATION: n=a or c or g or t
LOCATION: (360001)..(375000)
OTHER INFORMATION: n=a or c or g or t
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LOCATION: (270001)..(285000)
DTHER INFORMATION: n=a or c or g or t
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LCCATION: (49501)..(510000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc_feature
CCCATION: (510001)..(525000)
OTHER INFORMATION: n=a or c or g or t
                                                                                                                    NAME/KEY: misc_feature
LOCATION: (195001)..(210000)
OTHER INFORMATION: n=a or c or g or
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LOCATION: (210001)..(225000)
OTHER INFORMATION: n=a or c or g or
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LOCATION: (285001)..(300000)
OTHER INFORMATION: n=a or c or g or
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OCATION: (37501)..(390000)
WHER INFORMATION: n=a or c or g or
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OCATION: (390001)..(405000)
THER INFORMATION: n=a or c or g or
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LOCATION: (455001)..(465000)
OTHER INFORMATION: n=a or c or g or
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LOCATION: (465001)..(480000)
OTHER INFORMATION: n=a or c or g or
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LOCATION: (480001)..(495000)
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OTHER INFORMATION: n=a or c or g
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OCATION: (405001)..(420000)
THER INFORMATION: n=a or c or
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LOCATION: (22501)..(240000)
OTHER INFORMATION: n=a or c or
NAME/KEY: misc_feature
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THER INFORMATION: n=a or c or
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LCCATION: (300001)..(315000)
OTHER INFORMATION: n=a or c or
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THER INFORMATION: n=a or c or
                         INFORMATION: n=a or c or
                                                                LOCATION: (180001)..(195000)
OTHER INFORMATION: n=a or c or
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Sequence 1, Application US/09198452A

Patent No. 6552294

GENERAL INFORMATION:
APPLICANT: Griffais, R.
APPLICANT: Griffais, R.
TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, preve TITLE OF INVENTION: and treatment of infection
TITLE OF INVENTION: and treatment of infection
TITLE OF INVENTION: and treatment of infection
CURRENT APPLICATION NUMBER: US/09/198,452A
CURRENT FILING DATE: 1998-11-24

NUMBER OF SEQ ID NOS: 6849
                                              1086261 Gracecerraecesareces 1086311
                                                                                                                               1086372 GIGGTATGACTGAAGAATGCAAGCGATGTTTTATGGCGGGGGAATTCTATTTTCT 1086431
                                                                                                                                                                                                                                                                                                                                                 1086432 ATGGCGATAAATTACTTGTTACAGATAATCCAGAAGAAGATGGCGATCAGTTATTGATGG 1086491
                                                                                                                                                                                                1001 ATACAATGAAAGAGGCAGAACAGGTGATGTGCTTCATGGCTGGTTGTAATGCCATCTTCA 1060
                                                                                                                                                                                                                                                                                                1061 CAGGTAAGAAAATGCTCACAACAATGTGTAACGGCTGGGATGAGGATAAAGCCATGTTGG 1120
                                                                                                CCATTGCTACTGCAAGATTGGTCATGCCAACGTCTATTATCAGATTGGCTGCAGGAAGAT 1000
881 GCACGCCAATGTATGAAGAAGTTAAGAACAAGCAAGTTGAAGTTGAAGTTGATGATGTCAGAA 940
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NAME/KEY: misc_feature
LOCATION: (1).7(1500)
OTHER INPORMATION: n=a or c or g or t
NAME/KEY: misc_feature
LOCATION: (1500). (30000)
OTHER INPORMATION: n=a or c or g or t
NAME/KEY: misc_feature
LOCATION: (30001). (45000)
OTHER INPORMATION: n=a or c or g or t
NAME/KEY: misc_feature
LOCATION: (45001). (60000)
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LOCATION: (90001)..(105000)
OTHER INFORMATION: n=a or c or g or
NAME/KEY: misc feature
CACATION: (105001)..(120000)
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LOCATION: (120001)..(135000)
THER INFORMATION: n=a or c or g or
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OTHER INFORMATION: n=a or c or g or
NAME/KEY: misc_feature
LOCATION: (150001)..(165000)
OTHER INFORMATION: n=a or c or g or
NAME/KEY: misc_feature
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LOCATION: (60001)..(75000)
OTHER INFORMATION: n=a or c or g or
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THER INFORMATION: n=a or c or g or
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OTHER INFORMATION: n=a or c or
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ORGANISM: Chlamydia pneumoniae
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COCATION: (75001)..(900
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US-09-198-452A-1/c
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LOCATION: (88501)..(900000)
JTHER INFORMATION: n=a or c or g or t
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LOCATION: (58501)..(60000)
OTHER INFORMATION: n=a or c or g or
NAME/KEY: misc feature
LOCATION: (600001)..(615000)
OTHER INFORMATION: n=a or c or g or
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LOCATION: (66001)..(675000)
OTHER INFORMATION: n=a or c or g or
NAME/KEY: misc feature
LOCATION: (675001)..(690000)
OTHER INFORMATION: n=a or c or g or
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OCATION: (645001)..(660000)
OTHER INFORMATION: n=a or c or g or
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OCATION: (810001)..(825000)
OTHER INFORMATION: n=a or c or g or
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LOCATION: (630001)..(645000)
JTHER INFORMATION: n=a or c or g or
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THER INFORMATION: n=a or c or g or AME/KEY: misc_feature
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ACATION: (825001)..(840000)
THER INFORMATION: n=a or c or g or
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                                 LOCATION: (540001)..(555000)
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OTHER INFORMATION: n=a or c or g
NAME/KEY: misc_feature
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LOCATION: (55501). (570000)
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NAME/KEY: misc_feature
LOCATION: (57001)..(585000)
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THER INFORMATION: n=a or c or g
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COCATION: (76501)..(780000)
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1208704 TITCGATIAAAACIGGIGGATGCGTICAAGAIIGCGCCIACIGIGCCCAAICTICCGCI 1208645 1208824 CCTGGTCATTAGAAGACATCCGCGAAATTTATCACACTCCCGTATTTGAGCTGATTCACA 1208765 1208764 AAGCCAATGCCATATTGCGTAGTAATTTCCTCCATTCAGAACTGCAGACTTGCTATCTGA 1208705 1208585 1208525 1208524 AGG---ACGATCGATACTTTGATAGAGTCCTCGCTATGGTGAAAAGTATCACAGATCTCG 1208468 1208467 GAGCCGAGGTTTGTTGCTTTTAGGCATGCTCCCGAAGAGCAAGCTAAAAAACTGTATG 1208408 1208407 ATGCAGGACTTTATGCCTACAATCATAATTTAGACTCTTCTCCGGAATTCTATGAAACTA 1208348 1208347 TAATCACAACACGTTCTTATGAAGATCGCCTCAACACTCTTGATGTAGTAAATAATCTG 1208288 1208287 GCATTAGTACAGGCGGGGGGGGTATTGTAGGGAGAAATCTGAAGAAGACGGTATAAA 1208228 1208227 agcircircargretricaacaacaagaaricararcccagaarccgraccretaaarrrac 1208168 1208167 TTTGGCCGATTGACGGCACTTTGCAAGACCAGCCTCCGA------TTTCTTTCT 1208117 1208116 GGGAAGTCTTGCGAACCATAGCAACGGCACGGGTTGTTTTCCCCAGATCCATGGTACGAC 1208057 1207996 CCAACTCCATATTCTATGGAGATAAACTGTTGACTGTAGAAAACAATGATATAGATGAAG 1207937 1208056 TTGCTGCAGGACGCGCTTTCCTCACAGTAGAACAACAAACCTTATGTTTTCTAGCCGGTG 1207997 1045 865 GAATGGAGAGTTGTGTCACCCTGGGAATGGTTGATAAAGACCAAGCCACTGAATTGAAAA 625 1208584 AACGTGCTGTAGAGCTAGGCGCCACTCGTGTGTGTCTTGGGGGCTGCCTGGCGCAATGCTA GATTAAAGGCATGCACAGGTGGTATTCTTGGTCTTGGTGAGACCCAAGAGGACCGTGTAT 266 ATGCTCAGGTGCAACACAGAAGGTTCCAACAACCTTCAGAGGTTCAATTGTGCACTCTTA TGAATATCAAAACTGGTGGTTGTACCGAGGACTGTAAGTACTGTGCCCAATCACAGCGTT 386 ACAACACTGGTGTCAAGGCTGAAAGAATCATCCAAGTTGATGAGGTGATTGAAGCTGCAA 446 AGGAGGCAAAGGCCAATGGATCTACAAGGTTCTGTATGGGTGCTGCTTGGAGAGATGA GTGCTGGGTTGACGCGTACAACCATAACATTGATACTTACAAGGAACACTATCCAAAGG AAGGTAGAAAGTCAAAACTTGAAGAAAATCAAAGAGATGATCACTGCTGTCCATGACCTTG TGATCTCCACAAGAAGCTTTGATGATAGATTGAAAACATTCAAAAACGTTCAAGGATCTG 806 CTTTCCTCTACACCTTGGCCACAATGGATCAGCATCCAGAGTCTCTTCCAATCAACAGAC TGGCTGCAGGAAGATATACAATGAAAGAGGCAGAACAGGTGATGTGCTTCATGGCTGGTT 1046 GTAATGCCATCTTCACAGGTAAGAAATGCTCACAACAATGTGTAAACGGCTGGGATGAGG 926 ATGAGATTGTCAGAACCATTGCTACTGCAAGATTGGTCATGCCAACGTCTATTATCAGAT 12; Gaps Length 1230025; Indels Score 208.2; DB 4; Pred. No. 4.5e-54; 0; Mismatches 413; or g or ö 1207936 ATGCTGAAATGAT 1207924 17.5%; NAME/KEY: misc feature LOCATION: (900001)..(915000) OTHER INFORMATION: n=a or c NAME/KEY: misc_feature 1106 ATAAAGCCATGTT 1118 Query Match
Best Local Similarity 53.5'
Matches 488; Conservative 206 746 998 326 206 995 626 989 986 원 g ઠે ò g ઠે 8 ò 셤 ò 셤 ઠે 셤 Š g 셤 ò 셤 g 8 Š 8 ò ò ò ò

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APPLICANT: NIGHIO, Shoichi
APPLICANT: AKIMARU, Jiro
APPLICANT: AKIMARU, Jiro
APPLICANT: MITSHOW, Stockhi
TITLE OF INVENTION: Use of the Same
FILER REFERENCE: 0152-0490
CURRENT APPLICATION NUMBER: US/09/180,109A
CURRENT FILING DATE: 1998-12-03
PRIOR FILING DATE: 1997-03-03
NUMBER OF SEQ ID NOS: 52
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 23
LENGTH: 1420
TYPE: nw.
1198075 AGCTTCTTCATGTTCTTGCAACAGAGATCATATCCCAGAATCCGTACCTGTAAATTTAC 1198016
                                                                                                                                                     1198015 TTTGGCCGATTGACGCCACGCCTTTGCAAGACCAGCCTCCGA------TTTCTTTCT 1197965
                                                                                                                                                                                                                                                                                                          1197964 gggaagtrcrigcgaaccataccacaccecactecaccacateccacatecataccac 1197905
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                                                                                1046 GTAATGCCATCTTCACAGGTAAGAAAATGCTCACAAAATGTGTAAAGGCTGGGATGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1197844 CCAACTCCATATTCTATGGAGATAAACTGTTGACTGTAGAAACAATGATATAGATGAAG
                                                                                                                                                                                                                                  926 ATGAGATIGICAGAACCATIGCTACTGCAAGATIGGTCATGCCAACGTCTATTATCAGAI
                                                                                                                                                                                                                                                                                                                                                                                           TGGCTGCAGGAAGATATACAATGAAAGAGGCAGAACAGGTGATGTGCTTCATGGCTGGTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANIEM: Sphingomonas paucimobilis
FEATURE:
OTHER INFORMATION: Strain = JCM7511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1197784 ÁTGCTGAAÁTGAT 1197772
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LOCATION: (223)..(1245)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1198672 CCTGGTCATTAGAAGACATCCGCGAAATTTATCACACTCCCGTATTTGAGCTGATTCACA 1198613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1199612 AAGCCAATGCCATATTGCGTAGTAATTTCCTCCATTCAGAACTGCAGACTTGCTATCTGA 1198553
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1198552 TTTCGATTAAAACTGGTGGATGCGTTGAAGATTGCGCCTACTGTGCCCAATCTTCCCGCT
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                                                                                                                                                                                                                     APPLICANT: Stephens, Richard
APPLICANT: Stephens, Richard
APPLICANT: Stephens, Ralman, Sue
APPLICANT: Mitchell, Wayne
APPLICANT: Adlman, Sue
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Chlamydia Pneumoniae Genome Sequence
FILE REFERENCE: 018941-000411US
CURRENT APPLICATION NUMBER: US 60/108,279
PRIOR APPLICATION NUMBER: US 60/108,279
PRIOR APPLICATION NUMBER: US 60/128,606
PRIOR PILING DATE: 1998-11-12
PRIOR PILING DATE: 1999-04-08
NUMBER OF SEQ ID NOS: 1074
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 17.5%; Score 208.2; DB 4; Length 1 Best Local Similarity 53.5%; Pred. No. 4.5e-54; Matches 488; Conservative 0; Mismatches 413; Indels
                                                                                                                 Sequence 1, Application US/09438185A Patent No. 6822071 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Chlamydia pneumoniae
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                                            RESULT 14
US-09-438-185A-1/c
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                                                                                                                                                                     547 GGCGCGGCTGGCGCAACCCCAAGGATCG-----CGACATGCCCGCCATCGTGGAGATG 600
487 CGCGCCGTGCTGCAGGCGGCGCGCAGGCCAAGGATCACGGCTCGACGCGTTCTGCATG 546
                                                                                                                                                                                                                                                                                                                                                                 604 GACCAAGCCACTGAATTGAAAAGTGCTGGGTTGACGGCGTACAACCATAACATTGATACT 663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      661 GCACAGGCGCAGACGCTCGCCGAGGCGGGCTGGCTATTACAATCACAATATCGACACG 720
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                                                                                                                                                                                                                                                                            544 ATCACTGCTGTCCATGACCTTGGAATGGAGAGTTGTGTCACCCTGGGAATGGTTGATAAA 603
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                                                                                         484 GGTGCTGCTTGGAGAGAGATGAAAGGTAGAAAGTCAAACTTGAAGAAAATCAAAGAGATG
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September 17, 2005, 17:54:15; Search time 912 Seconds (without alignments) 8678.876 Million cell updates/sec
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| Cgn2_6/ptodata/2/pubpna/USO7_PUBCOMB.seq:*
| cgn2_6/ptodata/2/pubpna/USO6_MEW_PUB.seq:*
| cgn2_6/ptodata/2/pubpna/USO6_MEW_PUB.seq:*
| cgn2_6/ptodata/2/pubpna/USO6_PUBCOMB.seq:*
| cgn2_6/ptodata/2/pubpna/USO6_PUBCOMB.seq:*
| cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Sequence 1, Appli	Sequence 6038, Ap	Sequence 28355, A	Sequence 180438,	Sequence 29, Appl	Sequence 29, Appl	Sequence 1, Appli
SUMMARIES	ΠD	US-09-752-957B-1	US-10-741-849-6038	US-10-425-114-28355	US-10-425-115-180438	US-09-740-288A-29	US-10-431-544-29	US-10-390-472-1
	DB	10	21	18	20	0	16	18
	Query e Match Length DB ID	1188	1125	1334	1345	1659	1659	3083
de	Query Match	100.0	35.2	32.5	32.5	29.4	29.4	27.6
	Score	1188	417.6	386.2	386.2	349.2	349.2	328.2
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19 US-10-437-963-18311 9 US-09-740-288A-21	0-431-544	US-09-740-28	6 US-10-431-544	9 US-U9-74U-288A-23 16 TS-10-431-544-23	B IIS-10-425-114	US-10-425-115-719	7	6 US-10-431-544	7-701-13	-57	11 US-09-938-842A-579	1 US-10-702-364-1	9 US-09-740-288A-25		9 US-09-740-288A-11	16 US-10-431-544-11	æ	16 US-10-431-544-27	~	US-10-424-599-2	S-10-42	9 US-09-740-288A-19	16 US-10-431-544-19	9 US-09-740-288A-31	16 US-10-431-544-31	17 US-10-282-122A-8411	7 US-10-28	9 US-09-815-242-7073	-10-282-122A-22	17 US-10-282-122A-42017	-10-329-6	US-10-158-86	10-98	US-10-425-114-	17 US-10-312-273-284
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318.2	311.8								305.4	304	304	304	295.6	295.6	294.4	294.4	292.8	292.8	292.2	292.2	279.8	260.8	260.8	243.4	243.4	237.6	228.6	223.6	223.6	12.	211.6	211.6	211.6	210.4	208.2
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ALIGNMENTS

09-752-957B-1 equence 1, Application US/09752957B equence 1, Application US/09752957B ublication No. US20030104584A1 ENDERAL INFORMATION: APPLICANT: David SHIUAN APPLICANT: David SHIUAN APPLICANT: David SHIUAN APPLICANT: C. utilis BIO2 - biotin synthase CURRENT APPLICATION NUMBER: US/09/752,957B CURRENT APPLICATION NUMBER: US/09/752,957B NUMBER OF SEQ ID NOS: 1 ENGRIPH: 188 LENGTH. 188 TERMET HIS ACCORDED TO THE PREPARATION METHOD TO THE PREPARATION METHOD TO THE REPRESENCE TO THE PREPARATION METHOD TO THE			
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7B GH B: biot: /752,	Score 1188; DB 10; Length 1188; Pred. No. 0; 0; Mismatches 0; Indels 0;	1 AIGTCGTITATATTGACTGCTATTAGTCGTCCGATTGCTCTTTCCACTTCTAGAGTAGCT	61 TCTAGGGCTACTCTGGCAACAGGTGCTACTGCTGCGGAGATCTTGGAAGATGTGTTC 120
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99-752-9578-1 guence 1, Application US blication No. US20030104 NBEAL INFORMATION: PPLICANT: David SHIUMN ITLE OF INVENTION: YEAST TILE OF INVENTION: YEAST TILE OF INVENTION: VEAST URRENT FILING DATE: 200 URRENT FILING DATE: 200 URBER OF SEQ ID NOS: 1 OFFWARE: PATENTIN VERSION OFFWARE: PATENTIN VERSION LIBORATH: 1188 LIBORATH: 1188 TYPE: DNA ORGANISM: Candida utilis 0-752-9578-1	Simi]	ATG - -	5 5 5 5 5 5 7 5 7
9-752-9578-1 quence 1, Apquence 1, Apquence 1, Application No NERAL INFORM PEPLICANT: Dar ITLE OF INVE ILE OF INVE UNRENT FILIN UNRENT FILIN UNRENT FILIN UNRER: PAL Q ID NO 1 LANGTH: 1188 LANGTH: 1188 TYPE: DNA ORGANISM: Cal	Match ocal s 118		61
US-09-752-957B-1 Sequence 1, Application US/09752957B Publication No. US20030104584A1 GENERAL INFORMATION: APPLICANT: David SHIUAN TITLE OF INVENTION: YEAST WITH HIGH BIOTIN TITLE OF INVENTION: VEAST WITH HIGH BIOTIN CURRENT APPLICATION NUMBER: US/09/752,957B CURRENT APPLICATION NUMBER: US/09/752,957B CURRENT PILING DATE: 2003-01-10 SOFTWARE: Patentin version 3.1 SOFTWARE: Patentin version 3.1 SOFTWARE: Patentin version 3.1 SOFTWARE: DAA TYPE: DNA TYPE: DNA TYPE: DNA CORGANISM: Candida utilis US-09-752-957B-1	Query Match 100.0%; Best Local Similarity 100.0%; Matches 1188; Conservative		
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APPLICANT: Roemer, Terry
APPLICANT: Janey, Bo
APPLICANT: Janey, Bo
APPLICANT: Janey, Boone, Charles
APPLICANT: Bussey, Howard
TITLE OF INVENTION: Nucleic Acids Encoding Anti-fungal Drug Targets and Methods of TITLE OF INVENTION: NUMBER: US/10/741,849
CURRENT FILING DATE: 2003-12-19
PRIOR APPLICATION NUMBER: US 60/434,832
PRIOR FILING DATE: 2002-12-19
NUMBER OF SEQ ID NOS: 8000
SOFTWARE: Patentin version 3.2
SEQ ID NO 6038
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                                                                                                                                                                                                                                                                                                                                                                                                                              Score 417.6; DB 21;
Pred. No. 8.4e-116;
0; Mismatches 299;
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         Sequence 638, Application US/10741849
Publication No. US20050019931A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 35.2%;
Best Local Similarity 67.0%;
Matches 645; Conservative
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US-10-425-115-180438
US-10-425-115-180438
Sequence 180438, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rowai Thomas J.
APPLICANT: Exovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(5322)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT PILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 180438
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US-10-425-115-180438
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ORGANISM: 7
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Fublication No. US20040034888A1

GENERAL INPORMATION:
GENERAL INPORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Green, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21 (53313) B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
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   ACCGAGGACTGTAAGTACTGTGCCCAATCACAGGGTTACAACACTGGTGTCAAGGCTGAA 408
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US-10-425-114-28355
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ORGANISM: Zea mays
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LENGTH: 1334
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 Pred. No. 3.4e-106;
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APPLICANT: Kinney, Anthony
APPLICANT: Kinney, Anthony
APPLICANT: Miao, Guo-Hua
APPLICANT: Orozco, Emil
TITLE OF INVENTION: PLANT BIOTIN SYNTHASE
FILE REFERENCE: BB1439 US NA
CURRENT APPLICATION NUMBER: US 60/740,289A
CURRENT FILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: US 60/172929
PRIOR FILING DATE: 1999-12-21
NUMBER OF SEQ ID NOS: 36
SOFTWARE: Microsoft Office 97
SEQ ID NO 29 US/09740288A 29.4%; Query Match
Best Local Similarity 60.6
Matches 595; Conservative Sequence 29, Application U Patent No. US20010039042A1 TYPE: DNA
CORGANISM: Glycine max
US-09-740-288A-29 GENERAL INFORMATION: 833 g ò

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                                                                                                                                                                                                                                                                                                        ATGTGGATACGTCGAGGGTTTCTATCCCAAGGTTATCACGACCAGGACTTATGATGAGA
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TCAAAGAGATGATCACTGCTGTCCATGACCTTGGAATGGAGAGTTGTGTCACCCTGGGAA
                                                    rcaaaacaardecraaceaaarrceceaaareeerareeaaareeaaarareereeera
                                                                                                                         TGGTTGATAAAGACCAAGCCACTGAATTGAAAAGTGCTGGGTTGACGGCGTACAACCATA
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STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02173-4799
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATCHIN Release #1.0, Version #1.25
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APPLICATION NUMBER: US/10/390,472
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ADDRESSEE: HAMILTON, BROOF
STREET: Two Militia Drive
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US-10-390-472-1
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                                ATGAAGAAGTTAAGAACAAGCAAGTTGAAGTTGATGAGATTGTCAGAACCATTGCTACTG
                                                                                        AAGGA-----AACAAGAAGGTGGAATTTGAGAATATGTTGAGAATGGTTGCGACGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Allen, Steve
APPLICANT: Kinney, Tony
APPLICANT: Miao, Gou-Hua
APPLICANT: Orozco, Emil
TITLE OF INVENTION: PLANT BIOTIN SYNTHASE
FILE REFERENCE: BB1429 US NA
CURRENT APPLICATION NUMBER: US/10/431,544
CURRENT FILING DATE: 2003-05-07
PRIOR APPLICATION NUMBER: 60/172929
PRIOR FILING DATE: 1999-12-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGAAACCAATGGAGAGTTTCAA 1154
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SOFTWARE: Microsoft Office 97
SEQ ID NO 29
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; ORGANISM: Glycine max
US-10-431-544-29
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Best Local Similarity
Matches 595; Conserv
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APPLICANT: La Rosa, Thomas J.
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APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Boukharov, Andrey A.
APPLICANT: 38-21(5321)B
CURRENT FILING DATE: 2003-05-14
SEQ ID NO 18311
LENGTH: 1420
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Pred. No. 1.8e-85;
0; Mismatches 373; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Clone ID: PAT_MRT4530_23882C.1 US-10-437-963-18311
                                                                                                                                                 Sequence 18311, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
606 GAGGCATTTAAGTACGA 622
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Best Local Similarity 59.5%;
Matches 561; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: 1292..2590
OTHER INFORMATION: /product='"zuotin"
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                             PRIOR APPLICATION DATA:

PRIOR APPLICATION NUMBER: US/08/293,284
FILING DATE: 22-Aug. 1994
APPLICATION NUMBER: 07/973,326
FILING DATE: 28-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Brook, David E.
RECISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: MIT-600BA
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 3083 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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MOLECULE TYPE: DNA (genomic)
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Best Local Similarity 72.1'
Matches 445; Conservative
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Pred. No. 1.6e-83;
0; Mismatches 377;
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APPLICANT: Allen, Steve
APPLICANT: Miao, Gou-Hua
APPLICANT: Miao, Gou-Hua
TITLE OF INVENTION: PLANT BIOTIN SYNTHASE
FILE REFERENCE: BB1429 US NA
CURRENT APPLICATION NUMBER: US/10/431,544
CURRENT FILING DATE: 2003-05-07
PRIOR APPLICATION NUMBER: 60/172929
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; Sequence 21, Application US/10431544
; Publication No. US20030192073A1
; GENERAL INFORMATION:
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59.1%;
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SOFTWARE: Microsoft Office 97
SEQ ID NO 21
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Best Local Similarity 59.1
Matches 557; Conservative
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US-10-431-544-21
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CTTATGAATATCAAAACTGGTGGTTGTACCGAGGACTGTAAGTACTGTGCCCAATCACAG 381
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Sequence 21, Application US/09740288A
Patent No. US2000039042A1
GENERAL INFORMATION:
APPLICANT: Allen, Stephen
APPLICANT: Kinney, Anthony
APPLICANT: Minney, Anthony
TITLE OF INVENTION: PLANT BIOTIN SYNTHASE;
FILE REFERENCE: BB1429 US NA
CURRENT APPLICATION NUMBER: US/09/740,288A
CURRENT FILING DATE: 2000-12-19
PRIOR FILING DATE: 1999-12-21
NUMBER OF SEQ ID NOS: 36
SOFTWARE: Microsoft Office 97
SEQ ID NO 21
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APPLICANT: Orozco, Emil
TITLE OF INVENTION: PLANT BIOTIN SYNTHASE
FILE REFERENCE: BB1429 US NA;
CURRENT APPLICATION NUMBER: US/09/740,288A
CURRENT FILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: US 60/172929
PRIOR FILING DATE: 1999-12-21
NUMBER OF SEQ ID NOS: 36
SOFTWARE: Microsoft Office 97
SEQ ID NO 17
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RESULT 11 2.09-740-288A-17 Sequence 17, Application US/09740288A Patent No. US20010039042A1

GENERAL INFORMATION:
APPLICANT: Allen, Stephen
APPLICANT: Kinney, Anthony
APPLICANT: Miao, Guo-Hua

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ORGANISM: Hordeum vulgare
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LENGTH: 1396
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                                                                                                                            GTATCTTTCCTCTACACCTTGGCCACAATGGATCAGCATCCAGAGTCTCTTCCAATCAAC 861
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APPLICANT: Kinney, Anthony
APPLICANT: Kinney, Anthony
APPLICANT: Miao, Guo-Hua
TITLE OF INVENTION: PLANT BIOTIN SYNTHASE
FILE REFERENCE: BB1429 US NA
CURRENT APPLICATION NUMBER: US/09/740, 288A
CURRENT FILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: US 60/172929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 23, Application US/09740288A; Patent No. US20010039042A1; GENERAL INFORMATION:
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SOFTWARE: Microsoft Office 97
SEQ ID NO 23
LENGTH: 1439
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; ORGANISM: Zea mays
US-09-740-288A-23
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59.0%; Pred. No. 4.8e-83;
ive 0; Mismatches 378; Indels
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APPLICANT: Miao, Gou-Hua
APPLICANT: Miao, Gou-Hua
APPLICANT: Orozco, Emil
TITLE OF INVENTION: PLANT BLOTIN SYNTHASE
FILE REFERENCE: BB1429 US NA
CURRENT APPLICATION NUMBER: US/10/431,544
CURRENT FILING DATE: 1999-12-21
PRIOR APPLICATION NUMBER: 60/172929
PRIOR FILING DATE: 1999-12-21
NUMBER OF SEO ID NOS: 36
SOFTWARE: Microsoft Office 97
SEQ ID NO 17
                                                                                                                                                                                                                                                                                                                                        ; Sequence 17, Application US/10431544; Publication No. US20030192073A1; GENERAL INFORMATION:
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ORGANISM: Hordeum vulgare
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US-10-431-544-17
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RESULT 15
US-10-425-114-28968
Sequence 28968, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
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                                        GCAAAAAAGGCAAAAGAGTCTGGGAGCACCCGTTTTTGCATGGGAGCTGCATGGAGAGAA 534
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GCAAAGGAGCCAAAGGCCAATGGATCTACAAGGTTCTGTATGGGTGCTGCTTGGAGAGAG
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Publication No. US20030192073A1

GENERAL INFORMATION:
APPLICANT: Allen, Steve
APPLICANT: Kinney, Tony
APPLICANT: Miao, Gou-Hua
CURRENT APPLICATION NUMBER: US/10/431, 544
CURRENT FILING DATE: 1999-12-21

NUMBER: OF SEQ ID NOS: 36

SEQ ID NO 23

LENGTH: 1439
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US-10-431-544-23
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Local Similarity 59.0%; Fred. No. 4.8e-83;
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APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21(53313) B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 28958
LENGTH: 1486
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US-10-425-114-28968
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ORGANISM: Zea mays
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September 17, 2005, 15:54:19 ; Search time 4431 Seconds (without alignments) 10205.451 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Title: Perfect score: Sequence:	US-09-752-957F-1 1188 1 atgtegtttatattgaetgeaggttgeatteggtgettga 1188
Scoring table:	IDENTITY NUC Gapop 10.0 , Gapext 1.0
Searched:	34239544 segs, 19032134700 residues
Total number of	Total number of hits satisfying chosen parameters: 68479088
Minimum DB seq] Maximum DB seq]	Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : EST:*
1: 9D est1:*
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3: 9D htc:*
4: 9D est4:*
5: 9D est4:*
7: 9D est5:*
7: 9D est5:*
9: 9D 9ss1:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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1 333.4 28.1 969 CNSOGHEG ALA298894 2 330.4 25.8 9 CNSO6234 ALA298894 4 296.2 24.9 95.5 9 CNSO6234 ALA21814 5 294.4 24.9 95.5 9 CNSO73CQ ALA27092 6 29.2 24.9 95.5 9 CNSO73CQ ALA27092 7 291 24.6 14.2 3 CNSO49CQ BX818983 8 290.8 24.5 14.2 2004857 CO004857 CO0048519 9 25.2 24.5 87.6 7 CO084519 CO0048519 CO0048519 CO0048519 10 266 22.7 87.7 CC084519 CC084519 CC084519 11 26.2 22.1 87.7 CF22544 CF22544 CF22544 12 25.2 4 27.1 86.7 7 CF21966 CF721966 13 25.2 4 27.1 5 BU063672544 CF721966 <	;							
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25 233.4 19.6 509 26 23.3 19.6 644 28 231.4 19.6 644 29 229.2 19.3 664 31 227.4 19.1 596 33 225.6 19.1 707 34 221.9 18.5 891 35 219.8 18.5 891 36 219.8 18.5 891 37 216.2 18.2 730 38 206.6 17.4 766 41 204 17.2 831 42 201.2 16.9 588 44 199.4 16.8 681	AZ931212	AV923483	CA069980	BU062717	BU062716	CNSOGEOR	AV923288	AI960629	CF682132	CF719378	C0117806	AI775752	BU025073	CN145395	CA583129	BG582087	CD380074	CO136883	AW980387	CF449199	CB293284
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	19.6	19.6	19.6	19.5	19.3	19.2	19.1	19.1	19.0	18.6	18.5	18.3	18.2	17.4	17.3	17.2	17.2	17.1	16.9	16.8	16.8
•	233.4	233	232.4	231,4	229.2	228.6	227.4	226.6	225.2	221	219.8	217.2	216.2	206.6	206	204.2	204	203.2	201.2	199.4	199.2
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ALIGNMENTS

RESULT 1 CNSO6HEG LOCUS DEFINITION ACCESSION VERSION	CNSO6HEG 969 bp DNA linear GSS 30-NOV-2001 T7 end of clone ASOAA011H02 of library ASOAA from strain CLIB 533 of Saccharomyces bayanus, genomic survey sequence.
KEYWORDS SOURCE ORGANISM	GSS. Saccharomyces bayanus Saccharomyces bayanus Eukaryota; Pungi; Ascomycota; Saccharomycotina; Saccharomycetes;
REFERENCE AUTHORS	Jaccharlowycecares; saccharlowycecaces; saccharlowyces. 1 (bases 1 to 969) Souciet, J.L., Aigle, M., Artiguenave, F., Blandin, G., Bolotin-Fukuhara, M., Bon, E., Brottier, P., Casaregola, S., de-Montigny, J., Dujon, B., Durrens, P., Lepingle, A., Llorente, B., Malpertuy, A., Neuveglise, C., Ozier-Kalogeropoulos, O., Potier, S.,
TITLE JOURNAL MEDLINE	Wandker, P. and Weissenbach, J. Genomic, C., Mesolower, L. Douver, T., Wandker, P. and Weissenbach, J. Genomic exploration of the hemiascomycetous yeasts: 1. A set of yeast species for molecular evolution studies FEBS Lett. 487 (1), 3-12 (2000)
PUBMED REFERENCE AUTHORS TITLE	11152876 2 (bases 1 to 969) 2 (bases 1 to 969) Bon, E., Neuveglise, C., Casaregola, S., Artiguenave, F., Wincker, P., Aigle, M. and Durrens, P. Genomic exploration of the hemiascomycetous yeasts: 5.
JOURNAL MEDLINE PUBMED REFERENCE AUTHORS TITLE JOURNAL	Submitted (07-SEP-2000) Genoscope - Centre National de Sequencage,
COMMENT	2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail: seqrate@genoscope.cns.fr - Web: www.genoscope.cns.fr) This GSS is part of a random genomyc sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii, Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces accharomyces rouxii, Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces accharomyces rouxii, Saccharomyces hansenii zysomacharomyces rouxii, Saccharomyces hansenii var. hansenii, Pichia sorbitophila, Candida troplicalis and Yarrowia lipolytica. Genomic inserte of 3 to be were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of

FEATURES

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Genoscope.

Direct Submission

Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage,

Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage,

2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail:

seqretégenoscope.cns.fr - Web: www.genoscope.cns.fr)

This GSS is part of a random genomic sequencing program of thirteen
yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces
exiguus, Saccharomyces servazzii, Zygoasccharomyces touxii,
Saccharomyces kluyveromyces thermotolerans, Kluyveromyces
lactis var. lactis, Kluyveromyces thermotolerans, Kluyveromyces
lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia
angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila,
candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to
5 kb were prepared and both extremities were sequenced. See
by the sequence of this sequence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(<1. .>788)
/note="similar to Saccharomyces cerevisiae ORF YGR286c [
BIO2 ; biotin synthetase ]
                                                            Bukaryota; Pungi; Asconardans; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Kluyveromyces.

1 (bases 1 to 985)

2 ouciet, J.L., Aigle, M., Artiguenave, F., Blandin, G., Bolotin-Fukuhara, M., Bon, E., Brottier, P., Casaregola, S., Bolotin-Fukuhara, M., Dujon, B., Burrens, P., Lepingle, A., Libernte, B., Malpertuy, A., Dujon, B., Durrens, P., Lepingle, A., Libernte, B., Malpertuy, A., Neuveglise, C., Oziet-Kalogeropoulos, O., Porier, S., Saurin, W., Teksala, F., Toffano-Nioche, C., Wesolowski-Louvel, M., Wincker, P. and Weissenbach, J.

Senomic exploration of the hemiascomycetous yeasts: 1. A set of yeast species for molecular evolution studies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Malpertuy, A., Llorente, B., Blandin, G., Artiguenave, F., Wincker, P. and Dujon, B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        167 CATTGGAATATGCATTGTCAGTGAAGACACCAGTCAACACCTGGACCAAAGAAATTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Kluyveromyces thermotolerans"
/mol_type="genomic DNA"
/strain="CBS 6340"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27.8%; Score 330.4; DB 9;
larity 66.0%; Pred. No. 3.2e-82;
Conservative 1; Mismatches 252;
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/evidence=not_experimental
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Location/Qualifiers
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/clone="AY0AA015C04"
                      Kluyveromyces thermotolerans Kluyveromyces thermotolerans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kluyveromyces thermotolerans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone lib="AY0AA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              484 TGGTCGTTACACAATGAAGGAGCCGAACAATTTGTCTGCTTCATGGCTGGTTGTAACAG 543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     603
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    124 ATACAACCATAACATTGATACCTCCAGAGAACATTACAGTAAAGTCATCACCACAGAAC 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        761
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AL421814.1 GI:12205009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTACAACCATAACATTGATACTTACAAGGAACACTATCCAAAGGTGATCTCCACAAGAAG 701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63
                                                                                                                                                                                                                                                                                               <2. .>658
/note="similar to Saccharomyces cerevisiae ORF YGR286c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             522 CTTGAAGAAATCAAAGAGATGATCACTGCTGTCCATGACCTTGGAATGGAGAGTTGTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CATGAAGAGAATTGAGGAGATGATTTCRAAAGTGAACGACATGGGGCTGGAAACATGTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      582 CACCCTGGGAATGGTTGATAAAGACCAAGCCACTGAATTGAAAAGTGCTGGGTTGACGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                244 recresiarcriascriciascreaasceaasarcaccaritestricarriacaceri
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            364 GACTCCAATGGCTGAGGAACTTGCCGACCAGGAAGTAGAAGTTGCAATTCGATGAAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGTCAGAACCATTGCTACTGCAAGATTGGTCATGCCAACGTCTATTATCAGATTGGCTGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 333.4; DB 9; Length
Pred. No. 4.4e-83;
1; Mismatches 177; Indels
                                                                                  organism="Saccharomyces bayanus"
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     extremity of this insert.
Location/Qualifiers
                                                                                                                                                          /variety="uvarum"
/db.xref="taxon:4931"
/clone="ASOAA011H02"
/clone lib="ASOAA"
/note="end : T7"
                                                                                                      /mol_type="genomic DNA"
/strain="CLIB 533"
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V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C., Schachter V., Weissenbach J., Salanoubat M.
URGV INRA. Clepet C., Caboche M.
Annotation is based on the June 2003 version of the Arabidopsis genome released by MIPS (Munich Information center for Protein Sequences). 5 prime and 3 prime are assembled with Phrap.
http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_BF/Full_length
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                                                                                                                                                                                                           http://www.genoscope.cns.fr/cgi-bin/ggb/ggb?source=Arabidopsis.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CACTATGCTCAGGTGCAACACAGAAGGTTCCAACAACCTTCAGAGGTTCAATTGTGCACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTTATGAATATCAAAACTGGTGGTTGTACCGAGGACTGTAAGTACTGTGCCCCAATCACAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATGAAAGGTAGAAAGTCAAACTTGAAGAAAATCAAAGAGATGATCACTGCTGTCCATGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CGTTACAACACTGGTGTCAAGGCTGAAAGAATCATCCAAGTTGATGAGGTGATTGAAGCT
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Llarity 58.7%; Pred. No. 1.1e-72;
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Arabidopsis thaliana Full-length cDNA Complete sequence from clone GSLFTEF57ZGOS of Flowers and buds of strain col-0 of Arabidopsis bx819210
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BX81210.1
HTC; GSLT_CDNA.
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

I (bases I to 1301)
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Direct Submission
Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
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Life Technologies (a division of Invitrogen) members carried out
full-length libraries construction : Temple G.
Genoscope members carried out sequencing and annotation : Castelli
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Arabidopsis thaliana Full-length cDNA Complete sequence from clone GSLTFB34ZB08 of Flowers and buds of strain col-0 of Arabidopsis thaliana (thale cress).
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Arabidopsis thallana (thale cress)
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Spermatophyta, Magnoliophyta; eudicotyledons; core eudicots;
Trosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                /clone="BAQAB016H11"
/clone lib="BAQAB0"
complement(<13. ->689)
/note="similar to Saccharomyces cerevisiae ORF YGR286c
BIO2 ; biotin synthetase }"
/evidence=not_experimental
                                                                                                                                                                                                                                                                                                                                                                                  TATGACACACACTCATGGACTTGATGCACTATGCTCAGGTGCAACACAGAAGGTTCCAA
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5; Mismatches 204; Indels
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Direct Submission

Direct Submission

Submitted (08-58P-2000) Genoscope - Centre National de Sequencage,

2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail:

2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail:

FINIS GSS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces

exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii, Saccharomyces servazzii, Zygosaccharomyces rouxii, Saccharomyces kluyveromyces marxianus var. marxianus, Pichia angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila, Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to keywords for description of this sequence and for the sequence of the other extremity of this insert.

Location/Qualifiers
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Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetels;
Saccharomycetales; Saccharomycetales;
Saccharomycetales; Saccharomycetales;
E loases 1 to 955)
Souciet,J.L., Aigle,M., Artiguenave,F., Blandin,G.,
Bolotin-Fukuhara,M., Bon,E., Brottier,P., Casaregola,S.,
de-Montigny,J., Dujon,B., Durrens,P., Lepingle,A., Llorente,B.,
Malpertuy,A., Neuveglise,C., Ozier-Kalogeropoulos,O., Potier,S.,
Saurin,W., Tekaia,F., Toffano-Nioche,C., Wesolowski-Louvel,M.,
Wincker,P. and Weissenbach,J.
Genomic exploration of the hemiascomycetous yeasts: 1. A set of
yeast species for molecular evolution studies
L FEBS Lett. 487 (1), 3-12 (2000)
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                                                                956 ATATGGGAGATGATCAGGATGATTGGAACCGCACGTATTGTAATGCCAAAAGCGGATGGTG 1015
                                                                                                                                                                                                                                               CNS0735Q 955 bp DNA linear GSS 07-JUL-2001
clone BA0AB016H11 of library BA0AB from strain CLIB 210 of
                                                                                                                                                                                                     GGTTGTAATGCCATCTTCACAGGTAAGAAATGCTCACAACAATGTGTAACGGCTGGGAT
                       GITGATGAGATTGTCAGAACCATTGCTACTGCAAGATTGGTCATGCCAACGTCTATTATC
                                                                                                             AGATTGGCTGCAGGAAGATATACAATGAAAGAGGCAGAACAGGTGATGTGCTTCATGGCT
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Bolotin-Pukuhara,M., Toffano-Nioche,C., Artiguenave,F.,
Buchareau-Nguyen,G., Lemaire,M., Marmeisse,R., Montrocher,R.,
Robert,C., Termier,M., Wincker,P. and Wesolowski-Louvel,M.
Genomic exploration of the hemiascomycetous yeasts: 11.
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AL427092
AL427092.1 GI:12210286
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Submitted (15-APR-2002) Maize Mapping Project, University of
Missouri, Columbia, MO 65211, USA
Missouri, Columbia, MO 65211, USA
If you are interested in getting corresponding physical clones,
these are publicly available from ZmDB and may be found by BLAST
searching at MSL, maizemap.org; ZmDB, www.zmdb.iastate.edu; TIGR,
www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the
maize cDNA sequences is either Virginia Walbot, Stanford or Pat
Schnable, lowa State, then clones may be requested from ZmDB:
www.zmdb.iastate.edu.
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
                                                                                        639 AAGAAGGCTGGCCTCACTGCTTATAACCACAATCTTGATACTTCAAGAGAGTACTACCCA
                                                        AAGGTGATCTCCACAGAAGCTTTGATGATAGATTGAAAACATTCAAAAACGTTCAAGGA
                                                                                                                                                TCTGGATTAAAGGCATGCACAGGTGGTATTCTTGGTCTTGGTGAGACCCAAGAGGACCGT
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                                                                                                                                                                                                                                              802 GTATCTTTCCTCTACACCTTGGCCACAATGGATCAGCATCCAGAGTCTCTTCCAATCAAC
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Hainey, C.F., Dolan, M., Miao, G.H., Vogel, J.M., Whitsitt, M.S., Arthuri, L.W., Hanafey, M., Morgance, M. and Tingey, S.V.
Maize Mapping Project/DuPont Consensus Sequences for Design Covergo Probes
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/clone lib="Maize Mapping Project/DuPont Cornsensus
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/db_xref="MaizeDB:632870"
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Zea mays CL765_1 mRNA sequence.
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The sequences are based on single pass reads.
Life Technologies (a division of Invitrogen) members carried out full-length librairies construction : Temple G. Genoscope members carried out sequencing and annotation : Castelli V. Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C., Schachter V., Weissenbach J., Salanoubat M. URGV INRA : Clepet C., Caboche M.
Annotation is based on the June 2003 version of the Arabidopsis genome released by MIPS (Munich Information center for Protein Sequences). 5 prime and 3 prime are assembled with Phrap.
Castelli, V., Aury, J.M., Jaillon, O., Wincker, P., Clepet, C., Menard, M., Cruaud, C., Quet, er, F., Scarpelli, C., Schachter, V., Temple, G., Caboche, M., Weissenbach, J. and Salanoubat, M. Whole Genome Sequence Comparisons and 'Full-Length' Changach A Combined Approach to Evaluate and Improve Arabidopsis Genome
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/strain="Col-0"
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/note="this sequence is part of a project of EST assemblies resulting from the application of public contigs to seed DuPont contigs; this resource was assembled by DuPont as part of a collaboration for the overgo addressing of BACs in conjunction with the Maize Mapping Project"
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24.6%; Score 292; DB 3; Length 14
Best Local Similarity 55.2%; Pred. No. 2.9e-71;
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DOUGHED / DEST 09-JUN-2004 BST793192 Coccidioides posadasii spherule CDNA library, 0.4 to 2.3 kb Coccidioides posadasii cDNA clone CIEAL82 5' end, mRNA sequence. CO004857
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Editaryota; Fungi, Ascomycota; Pezizomycotina; Eurotiomycetes;
Editaryota; Fungi, Ascomycota; Pezizomycotina; Eurotiomycetes;
Onygenales; mitosporic Onygenales; Coccidioides.

E 1 (bases 1 to 969)
S Gardner, M. J. and Cole, G.T.
Analysis of gene expression in Coccidioides posadasii mycelia and spherules via expressed sequence tags
Unpublished (2003)
Context: Gardner MJ
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301 838 9208
Email: gardner@tigr.org
Seq primer: M18 Reverse.
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0.4 to 2.3 kb"
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Score 291, DB 7; Length 96
Pred. No. 5e-71;
0; Mismatches 315; Indels
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/organism="Coccidioides
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Query Match Query Match Query Match Best Local Similarity 59.5%; Pred. No. 5.58-71; Matches 515; Conservative 0; Mismatches 342; Indels 9; Gaps 1; Qy 276 GCAACACAGAAGTTCCAACACTCAAGAGTTCTCATTGTACATTCTCCTCTCAATCAA	576 TTGTGTCACCTGGGAATGGTTGATAAAGACCAAGCCACTGAATTGAAAAGAGGTGTGGTT	Oy 936 CAGAACCATTGCTACTGCAAGATTGCTCATGCCAACGTCTATTATCAGATTGGTGGGG 995 Db 653 TCGGATGATTGCCACTGCTCGAAATGTGATGGTCAGGTTGTCAGCTGG 712 OY 996 AAGATATACATGCACTGCTCGAAACGGTGATTGTTTGTTGTTGTTGTTGTTGTTTTGTTGTTTTGTTTTGTTTT
	8 9 9 C 8 4	TITLE Global assembly of Cotton ESTS JOURNAL Unpublished (2004) COMMENT Contact: Rod A. Wing Arizona Genomics Institute The University of Arizona Forbes Bullding Room 303, Tucson, AZ, 85721-0036, USA Tel: 520 626 9595' Fax: 520 621 1259 Email: http://genome.arizona.edu Plate: 01 row: D column: 02. FEATURES Location/Qualifiers 1. 876 /organism="Gossypium raimondii" /mol_type="mRNA" = "Raxon: 29730" /db_txref="taxon: 29730" /db_tsref="taxon: 29730" /db_tsref="taxon: 29730" /db_tsref="bh10B" /db_tsref="bh10B" /db_tsref="bh10B" /db_tsref="bh10B" /clone lib="GR" Ea" /clone lib="GR" /clone lib="GR" Ea" /clone lib="GR" /clone lib="GR" Ea" /clone lib="GR" Ea" /clone lib="GR" Ea" /clone lib="GR" /clone lib="GR" Ea" /clone lib="GR" /clone lib="GR" Ea" /clone lib="GR" /clo

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CP822544
EST699926 Coccidioides posadasii saprobic phase cDNA library, 2 to 4 kb Coccidioides posadasii cDNA clone CIDAG50 3' end, mRNA
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library, 2 to 4 kb"
library, 2 to 4 kb"
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/cocidioides posadasii saprobic phase cDNA library, size
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bukaryota, Fungii Ascomycota, Pezizomycotina, Eurotiomycetes,
Onygenales, Fungii Ascomycota, Coccidioides.
1 (bases 1 to 834)
2achder, M.J. and Cole, G.T.
Analysis of gene expression in Coccidioides posadasii mycelia and
spherules via expressed sequence tags
643 ATCTTGACACGTCGAGAGAATTCTACCCATCCATCATCACCACGAGATCGTGAGGAGA
                                                                                                                                                GATTGAAAACATTCAAAAACGTTCAAGGATCTGGATTAAAGGCATGCACAGGTGGTATTC
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llarity 61.6%; Pred. No. 6.1e-64;
Conservative 0; Mismatches 270; Indels
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Other ESTS: EST69927
Contact: Gardner MJ
The Institute for Genomic Research
Tol. Medical Center Drive, Rockville, MD 20850, USA
Tel: 301 838 3519
Fax: 301 838 0208
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Location/Qualifiers
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etrain="C735"
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Seq primer: M13 Reverse.
                                                                   CF822545.1 GI:45928602
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Rockville, MD 20850, USA
Tel: 301-838-3543
                                                                                                                                                                                                                                910 AAGCAAGTTGAAGTTGATGAGATTGTCAGAACCATTGCTACTGCAAGATTGGTCATGCCA 969
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                                            GAACACTATCCAAAAGGTGATCTCCACAAGAAGCTTTGATGATAGATTGAAAACATTCAAA
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Cryptococcus neoformans var. neoformans
Eukaryota; Fungi; Basidiomycota; Hymenomycetes;
Heterobasidiomycetes; Tremellomycetidae; Tremellales;
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JEC21 cDNA library
Unpublished (2003)
Other ESTS: CCAIS17TR
Contact: Brendan Loftus
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CF721966.1 GI:41576125
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Email: crypt@tigr.org
Seq primer: TF.
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/db_xref="taxon:40410"
/clone="CQXIS17"
/clone="CQXIS17"
/note="Vector: pCMVSport6; Site_1: NotI_EcoRV; The full
length, normalized library was prepared from a variety conditions using RNA provided by Joseph Heltman and Jennifer Lodge"
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391 AAGGTCCACACCGTCCTCCGAACCATCGCTACTGCCTATCGTTCTTCCCAAGACCATC 332
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            329 ATATCAAAACTGGTGGTTGTACCGAGGACTGTAAGTACTGTGCCCAATCACAGCGTTACA 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 craraaagaceeereeereeareaagarierrerrarreceereaarerras 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (http://www.genoplante.com and http://genoplante-info.infobiogen.fr).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genoplante, a major partnership french program in plant genomics Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                               1099 GATGAGGATAAAGCCATGTTGGCTAAATGGGGTCTGAAACCAATGGAGAGTTTCAAATAC
                                                                                                                                                                                      331 ATTCGTCTCGCCGCTGGCCGACACGAATTCAGCGAGACCGAACAAGCCATGGCCTTCATG
                                                                                                                                                                                                                                                               1039 GCTGGTTGTAATGCCATCTTCACAGGTAAGAAAATGCTCACAACAATGTGTAACGGCTGG
                                                                                                                                                                                                                                                                                                            GAGCTCAAGTTCATAGACATGCTCAGAATTTTAGGGAGGTTCAGCAGTGTACGCTTCTGT
                                                                                                              ATCAGATTGGCTGCAGGAAGATATACAATGAAAGAGGCAGAACAGGTGATGTGCTTCATG
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Helianthus annuus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheol
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; campanulids; Asterales; Asteraceae; Asteroideae;
Heliantheae; Helianthus.
1 (bases 1 to 781)
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/clone="HaDBevR27F09"
/tissue_type="t days after self-pollination embryo"
/clone_lib="HaDevRs"
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Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21.2%; Score 251.6; DB 6; 58.5%; Pred. No. 7.3e-60;
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/cultivar="psc8"
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Genoplante
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Department of Bukaryotic Genomics, TIGR, 9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-3543
Fax: 301-838-0208
Email: crypt@tigr.org
Seq primer: TF
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                                                                                                                                                                                          Bukaryota; Fungi, Basidiomycota; Hymenomycetes;
Heterobasidiomycetes; Tremellomycetidae; Tremellales; Tremellaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:40410"
/dc]one="CCADET16"
/clone lib="C.neoformans strain JEC21"
/note="Vector: pCMVSport6; Site_1: NotI_ECORV; The full
/note="vector: pcmvs.com"/ site_1: NotI_ECORV; The full
/notice="vector: pcmvs.com"/ site_1
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                                                                                   Cryptococcus neoformans var. neoformans (Filobasidiella neoformans
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|mol_type="mRNA"
|strain="JEC21"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6
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                                                                                                                                                                                                                                                                                                                                                                             from a Full length enriched,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21.2%; Score 252.4; DB 7; Length llarity 60.5%; Pred. No. 4.5e-60; Conservative 0; Mismatches 276; Indels
                                                                                                                                                            neoformans
                                                                                                                                                               var.
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JEC21 CDNA library
Unpublished (2003)
Other ESTS: CCAEFIGTR
Contact: Brendan Loftus
                                                                                                                         var. neoformans)
Cryptococcus neoformans
               GI:41573535
                                                                                                                                                                                                                                                                                                     (bases 1 to 862)
                                                                                                                                                                                                                                                                      Filobasidiella.
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                                                                                                                                                                                                                                                                                                                                       Loftus, B.
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Best Local S
Matches 437
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                                                                                                                                                                                                                                                                                              CCATGACCTTGGAATGGAGGTTGTCACCCTGGGAATGGTTGATAAAGACCAAGCCAC 614
                                                                                                                                                                                                                                                                                                                               CAAGGGCATGGGAATGGAGGTCTGCGTAACGCTGGGCATGATCGACGCGGAGCAGGCCAA 637
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Strabidopsis thaliana
Strabidopsis viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots;
rosids; eurosids II; Brassicales; Erassicaceae; Arabidopsis.
(bases 1 to 671)
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Lundsgaard, M., Emmersen, J., Nielsen, K.L., Wilson, I., Somerville, S.
                                 /mol_type="mRNA"
/strain="RREL 11084"
/db_xraon:5518"
/clone_lb="taxon:5518"
/clone_lb="Nitrogen-starved mycelia"
/note="Vector: Uni-ZapII; Site_1: EcoRI; Site_2: XhoI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1151
                                                                                                                                                                                                                                                          GAGGGACATGCGCGGACGAGAACAGCCTCAAGAACATCAAGGCCCATGGTCGAGGGCGT
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                                                                                                                                                         Length 770;
                                                                                                                                                       Score 251.4; DB 5; Length
Pred. No. 8.3e-60;
0; Mismatches 236; Indels
                      zeae"
                     organism="Gibberella"
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llarity 62.7%;
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ACACTGGGGCAAGGAAGAAGAATCATCCAAGTTGATGAGGTGATTGAAGCTGCAAAGG 448
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Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.

1 (bases 1 to 770)
Trail,F., Xu,J.-R., San Miguel,P., Halgren,R.G. and Kistler,H.C.
Analysis of expressed sequence tags from Gibberella zeae (anamorph Fusarium graminerium, 2, 1, 107-107 (2003)
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                                                                                                                                                                                                                                                                                              CAGGCCTTACAGCTTACAATCATAACCTTGATACATCAAGAGAGTACTACCTAATATCA
                              ATACTGGAGTGAAAGCTCATGAACAAGATGCTCTTCTTGAAGCTGCACAAA
                                                                   GTAGAAAGTCAAACTTGAAGAAAATCAAAGAGATGATCACTGCTGTCCATGACCTTGGAA
                                                                                                                                                                       GAAGGAAAACCAACTTTAGTCAGATCCTTGAATATGTGAAAGAGAGATAAGGGGTATGGGAA
                                                                                                                                                                                                       TGGAGAGTTGTGTCACCCTGGGAATGGTTGATAAAGACCAAGCCACTGAATTGAAAAGTG
                                                                                                                                                                                                                                       CTGGGTTGACGGCGTACAACCATAACATTGATACTTACAAGGAACACTATCCAAAGGTGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      <u> AGATGATACCGATGATTGCTACGGCCCGCATCACGATGCCGAAAGCTATGGTGAGGTTAT</u>
                                                                                                                                                                                                                                                                                                                                           TCTCCACAAGAAGCTTTGATGATAGATTGAAAACATTCAAAAACGTTCAAGGATCTGGAT
                                                                                                                                                                                                                                                                                                                                                                                                               TAAAGGCATGCACAGGTGGTATTCTTGGTCTTGGTGAGACCCAAGAGGACCGTGTATCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Department of Plant Biology Michigan State University East Lansing, MI 48824, USA Tel. 517 432 2939 Fax: 517 353 1926 Email: trail@msu.edu Plate: 3 row: G column: 19. Location/Qualifiers
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/db xrefe="carmings"
/db xrefe="carmings"
/dev_stage="Plant 3 weeks old, three days post infection"
/dev_stage="Plant 3 weeks old, three days post infection"
/clone lib="infected Arabidopsis Leaf"
/note="Organ: Leaf; Vector: pBluescript; Mixed cDNA
library of Arabidopsis and E. cichoracearum infected leaf
from three weeks old Arabidopsis plants. Plants were
harvested 3 days after infection and mRNA oligo dT
selected."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         306 GGTTCAATTGTGCACTCTTATGAATATCAAAACTGGTGGTTGTACCGAGGACTGTAAGTA 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 271 TAGTGGGGTTCGAAGTTTGGGTATGGAATGTTGTGTGACGCTAGGAATGATCGACCTTGA 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  331 GCAGGCAAAAGAATTAAAAGAGGCAGCTTGACAGCATATAATCATAATGTCGATACATC 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              366 CTGTGCCCAATCACAGCGTTACAACACTGGTGTCAAGGCTGAAAGAAGCATCATCCAAGTTGA .425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    91 rigiecrcaarcricacrargaracagarraaageccaccaagargaacrerrea 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             426 TGAGGTGATTGAAGCTGCAAAGGAGGCAAAGGCCAATGGATCTACAAGGTTCTGTATGGG 485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             151 CTCTGTCCTAGAAGCAGCCAAAATTGCGAAAAGTAACGGTAGCACAAGATTCTGTATGGG 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         211 TGCGGCTTGGAGAGACATGCGAGGACGAAAGTCGGGCTTGAAGAACATCAAGGAAATGGT 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               546 CACTGCTGTCCATGACCTTGGAATGGAGGTTGTCTCACCCTGGGAATGGTTGATAAAGA 605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         726 CAAAAACGTTCAAGGATCTGGATTAAAGGCATGCACAGGTGGTATTCTTGGTCTTGGTGA 785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    786 GACCCAAGAGGACCGTGTATCTTTCCTCTACACCTTGGCCACAATGGATCAGCATCCAGA 845
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                666 CAAGGAACACTATCCAAAGGTGATCTCCACAAGAAGCTTTGATGATAGATTGAAAACATT 725
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31 GATCCAGATGTGTACACTCATGAACATCAAAACTGGTGGCTGTAGCGAAGATTGCTCTTA 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGCTGCTTGGAGAGAGATGAAAGGTAGAAAGTCAAACTTGAAGAAAATCAAAGAGATGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  391 AAGGGAACACTACCCCTCAGTAATAACTACTCGAACCTACGATGAGCGACTTCAAACTAT
Welinder, K.G. sequencing of Erysiphe cichoracearum infected Arabidopsis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21.1%; Score 250.2; DB 6; Length 671; 64.0%; Pred. No. 1.7e-59; ive 0; Mismatches 213; Indels 0
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formate: Karen G. Welinder
Contact: Karen G. Welinder
Institut for bioteknologi
Aalborg Universitet
Schngaardsholmsvej 49, 9000 Aalborg, Denmark
Tel: 445 98141808
Fax: 445 98141808
Email: kgw@bio.auc.dk.
Location/Qualifiers
...Annsis thaliana"
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Corganisma-"Arabidopsis thaliana"
/mol type="mRNA"
/ecoType="Columbia"
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Best Local Similarity 64.0
Matches 378; Conservative
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COMMENT
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Search completed: September 17, 2005, 19:08:06 Job time : 4438 secs